



```

61 RPRMGAAPASAPHMNETAEKNLGVLADEDNLTQONSSNISYSNAMOKEITLPSRLIY 120
QY 121 INDESESPYHVLDTKARHOKHKNKAVHLAASFOIEAFSGKFTLIDLINNGLLSSDYVEI 180
Db 121 INDESESPYHVLDTKARHOKHKNKAVHLAASFOIEAFSGKFTLIDLINNGLLSSDYVEI 180
QY 181 HYENKGPQYSGKGHECHYHGSIRGVDSKVALSTCNGLHGMFEDDTFVYMIPELVLHDE 240
Db 181 HYENKGPQYSGKGHECHYHGSIRGVDSKVALSTCNGLHGMFEDDTFVYMIPELVLHDE 240
QY 241 KSTGRPHIIOKTLAGQYSKOMKMLTMRGDMPFLSELQMLKRRKRAVNSRGIFPEEMKY 300
Db 241 KSTGRPHIIOKTLAGQYSKOMKMLTMRGDMPFLSELQMLKRRKRAVNSRGIFPEEMKY 300
QY 301 LELMIVNDHKTYYKHHSSHAHTNNFAKSVNLVDSIYKQOLNTRVYLVAETWTEKQID 360
Db 301 LELMIVNDHKTYYKHHSSHAHTNNFAKSVNLVDSIYKQOLNTRVYLVAETWTEKQID 360
QY 361 ITTNPVOMLHEFSKYRQRIKOHADAVHLISRVTFFHRRSSLSYFGVCSRTRGVNEYG 420
Db 361 ITTNPVOMLHEFSKYRQRIKOHADAVHLISRVTFFHRRSSLSYFGVCSRTRGVNEYG 420
QY 421 LPMVAOVAVLSQSLAQNGLIOWEPSSRRPKCDCTESMGCCIMEETGVSHSRKFSKSTLEY 480
Db 421 LPMVAOVAVLSQSLAQNGLIOWEPSSRRPKCDCTESMGCCIMEETGVSHSRKFSKSTLEY 480
QY 481 RDLFLORGGAGCLFNRPRTKLEPTECGNGYVEAGEEDCGFHEVCYGLCKKCSLSNGAHC 540
Db 481 RDLFLORGGAGCLFNRPRTKLEPTECGNGYVEAGEEDCGFHEVCYGLCKKCSLSNGAHC 540
QY 541 SDGPCNNNTSCLFOPRGYECRDVAVNECDITTEYCTGDSGQCPNMLHKODGYACONOGRCY 600
Db 541 SDGPCNNNTSCLFOPRGYECRDVAVNECDITTEYCTGDSGQCPNMLHKODGYACONOGRCY 600
QY 601 NECKTRDNOCYIWTGKAAGSDKFCYEKLNTEGTEKNGCKGDKGDMWIOCSKIDVFCGFL 660
Db 601 NECKTRDNOCYIWTGKAAGSDKFCYEKLNTEGTEKNGCKGDKGDMWIOCSKIDVFCGFL 660
QY 661 LCTNLTFRAPRIGOLOGEIIPTSFYHOGRYIDCSGAHVVLDDDTDVGYVEDGTPCGPSMNC 720
Db 661 LCTNLTFRAPRIGOLOGEIIPTSFYHOGRYIDCSGAHVVLDDDTDVGYVEDGTPCGPSMNC 720
QY 721 LDRKCLQIOALNMSSCPDLSKGVCSGHGVCSEATCICDFTWAGTDCSIRDPVRLNHP 780
Db 721 LDRKCLQIOALNMSSCPDLSKGVCSGHGVCSEATCICDFTWAGTDCSIRDPVRLNHP 780
QY 781 KDEGPKGPSATNLIIIGSITAGALIVAIIVLGCTGWMGFKNVKKRRRDPDQGP 832
Db 781 KDEGPKGPSATNLIIIGSITAGALIVAIIVLGCTGWMGFKNVKKRRRDPDQGP 832

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RESULT 2
US-09-791-537-64795
; Sequence 64795, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 64795
; LENGTH: 832
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-64795

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Query Match 100.0%; Score 4553; DB 21; Length 832;
Best Local Similarity 100.0%; Pred. NO. 0;

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Matches 832; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKPPGSSSRQPLPLAGCSLAGACGPGRGAGSVAPAPARTPCORILLVLLPLAASS 60
Db 1 MKPPGSSSRQPLPLAGCSLAGACGPGRGAGSVAPAPARTPCORILLVLLPLAASS 60
QY 61 RPRMGAAPASAPHMNETAEKNLGVLADEDNLTQONSSNISYSNAMOKEITLPSRLIY 120
Db 61 RPRMGAAPASAPHMNETAEKNLGVLADEDNLTQONSSNISYSNAMOKEITLPSRLIY 120
QY 121 INDESESPYHVLDTKARHOKHKNKAVHLAASFOIEAFSGKFTLIDLINNGLLSSDYVEI 180
Db 121 INDESESPYHVLDTKARHOKHKNKAVHLAASFOIEAFSGKFTLIDLINNGLLSSDYVEI 180
QY 181 HYENKGPQYSGKGHECHYHGSIRGVDSKVALSTCNGLHGMFEDDTFVYMIPELVLHDE 240
Db 181 HYENKGPQYSGKGHECHYHGSIRGVDSKVALSTCNGLHGMFEDDTFVYMIPELVLHDE 240
QY 241 KSTGRPHIIOKTLAGQYSKOMKMLTMRGDMPFLSELQMLKRRKRAVNSRGIFPEEMKY 300
Db 241 KSTGRPHIIOKTLAGQYSKOMKMLTMRGDMPFLSELQMLKRRKRAVNSRGIFPEEMKY 300
QY 301 LELMIVNDHKTYYKHHSSHAHTNNFAKSVNLVDSIYKQOLNTRVYLVAETWTEKQID 360
Db 301 LELMIVNDHKTYYKHHSSHAHTNNFAKSVNLVDSIYKQOLNTRVYLVAETWTEKQID 360
QY 361 ITTNPVOMLHEFSKYRQRIKOHADAVHLISRVTFFHRRSSLSYFGVCSRTRGVNEYG 420
Db 361 ITTNPVOMLHEFSKYRQRIKOHADAVHLISRVTFFHRRSSLSYFGVCSRTRGVNEYG 420
QY 421 LPMVAOVAVLSQSLAQNGLIOWEPSSRRPKCDCTESMGCCIMEETGVSHSRKFSKSTLEY 480
Db 421 LPMVAOVAVLSQSLAQNGLIOWEPSSRRPKCDCTESMGCCIMEETGVSHSRKFSKSTLEY 480
QY 481 RDLFLORGGAGCLFNRPRTKLEPTECGNGYVEAGEEDCGFHEVCYGLCKKCSLSNGAHC 540
Db 481 RDLFLORGGAGCLFNRPRTKLEPTECGNGYVEAGEEDCGFHEVCYGLCKKCSLSNGAHC 540
QY 541 SDGPCNNNTSCLFOPRGYECRDVAVNECDITTEYCTGDSGQCPNMLHKODGYACONOGRCY 600
Db 541 SDGPCNNNTSCLFOPRGYECRDVAVNECDITTEYCTGDSGQCPNMLHKODGYACONOGRCY 600
QY 601 NECKTRDNOCYIWTGKAAGSDKFCYEKLNTEGTEKNGCKGDKGDMWIOCSKIDVFCGFL 660
Db 601 NECKTRDNOCYIWTGKAAGSDKFCYEKLNTEGTEKNGCKGDKGDMWIOCSKIDVFCGFL 660
QY 661 LCTNLTFRAPRIGOLOGEIIPTSFYHOGRYIDCSGAHVVLDDDTDVGYVEDGTPCGPSMNC 720
Db 661 LCTNLTFRAPRIGOLOGEIIPTSFYHOGRYIDCSGAHVVLDDDTDVGYVEDGTPCGPSMNC 720
QY 721 LDRKCLQIOALNMSSCPDLSKGVCSGHGVCSEATCICDFTWAGTDCSIRDPVRLNHP 780
Db 721 LDRKCLQIOALNMSSCPDLSKGVCSGHGVCSEATCICDFTWAGTDCSIRDPVRLNHP 780
QY 781 KDEGPKGPSATNLIIIGSITAGALIVAIIVLGCTGWMGFKNVKKRRRDPDQGP 832
Db 781 KDEGPKGPSATNLIIIGSITAGALIVAIIVLGCTGWMGFKNVKKRRRDPDQGP 832

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RESULT 3
US-09-824-129-3
; Sequence 3, Application US/09824129
; GENERAL INFORMATION:
; APPLICANT: Lopez-Olin, Carlos
; APPLICANT: Miguel, Santiago Cal
; APPLICANT: Freije, Jose Maria Perez
; APPLICANT: Garcia, Jose Manuel Lopez
; APPLICANT: Bianchi, Albert Bernard
; APPLICANT: Trill, Pamela
; TITLE OF INVENTION: Methods and Compositions for Modulating
; FILE REFERENCE: D0015-NP
; CURRENT APPLICATION NUMBER: US/09/824,129

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CURRENT FILING DATE: 2001-04-02  
 PRIOR APPLICATION NUMBER: 60/194,164  
 PRIOR FILING DATE: 2000-04-03  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 3  
 LENGTH: 832  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-824-129-3

Query Match 100.0%; Score 4553; DB 22; Length 832;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 832; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKPPSSSRPPPLAGCSLAGASCGPORGAGSVASAPARTPPCRLLVLLPPLAAS 60  
 1 MKPPSSSRPPPLAGCSLAGASCGPORGAGSVASAPARTPPCRLLVLLPPLAAS 60  
 61 RPRAGAAAPAPAHNETAEKRLGVLADENLTLOONSSNISYSNAMOKEITLPSRLIY 120  
 61 RPRAGAAAPAPAHNETAEKRLGVLADENLTLOONSSNISYSNAMOKEITLPSRLIY 120  
 61 RPRAGAAAPAPAHNETAEKRLGVLADENLTLOONSSNISYSNAMOKEITLPSRLIY 120  
 121 INODESEYHVLDTKARHQQHKAHVAHQAQSFQIEAFGSKFLDLINNGLLSPYVEI 180  
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 181 HENKRPQYSGGEGHCYHGSIRGVKDSKVALSTCNGLHGFEDDTFYMMIEPELVHDE 240  
 181 HENKRPQYSGGEGHCYHGSIRGVKDSKVALSTCNGLHGFEDDTFYMMIEPELVHDE 240  
 181 HENKRPQYSGGEGHCYHGSIRGVKDSKVALSTCNGLHGFEDDTFYMMIEPELVHDE 240  
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 241 KSTGRPHIIOKTLAAGYSKOMKNTLMERGDOMPLSELQWLKRRKRAVNSRGIFEEMKY 300  
 241 KSTGRPHIIOKTLAAGYSKOMKNTLMERGDOMPLSELQWLKRRKRAVNSRGIFEEMKY 300  
 301 LELMIVNDHKTYYKRRSSHAHTNFAKSVNLVDSIYKEQLNTRVVAVEETWTEKDOID 360  
 301 LELMIVNDHKTYYKRRSSHAHTNFAKSVNLVDSIYKEQLNTRVVAVEETWTEKDOID 360  
 301 LELMIVNDHKTYYKRRSSHAHTNFAKSVNLVDSIYKEQLNTRVVAVEETWTEKDOID 360  
 361 ITTNPVQMLHFSKYRORIKOHADAVHLISRVTFFHYKRSLSYFGVGCRTGAVNEYG 420  
 361 ITTNPVQMLHFSKYRORIKOHADAVHLISRVTFFHYKRSLSYFGVGCRTGAVNEYG 420  
 361 ITTNPVQMLHFSKYRORIKOHADAVHLISRVTFFHYKRSLSYFGVGCRTGAVNEYG 420  
 421 LPMVAQVLSQSLAONLGIOWEPSSRRPKDCDCTESMGCCIMEETGVSHSRKFSKSILEY 480  
 421 LPMVAQVLSQSLAONLGIOWEPSSRRPKDCDCTESMGCCIMEETGVSHSRKFSKSILEY 480  
 421 LPMVAQVLSQSLAONLGIOWEPSSRRPKDCDCTESMGCCIMEETGVSHSRKFSKSILEY 480  
 481 RDLFLOGGGACLFNRPKLEPTEECGNGYVEAGEECDCGFHVECYGLCKKCSLSNGAHC 540  
 481 RDLFLOGGGACLFNRPKLEPTEECGNGYVEAGEECDCGFHVECYGLCKKCSLSNGAHC 540  
 481 RDLFLOGGGACLFNRPKLEPTEECGNGYVEAGEECDCGFHVECYGLCKKCSLSNGAHC 540  
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 541 SDGPCCNTSCLFOPRGYECRDVAVNECDITEYCTGDSGCPNHLKHODGYACNOGRCY 600  
 541 SDGPCCNTSCLFOPRGYECRDVAVNECDITEYCTGDSGCPNHLKHODGYACNOGRCY 600  
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 601 NGECKTRDNOCQYIWTGKAAGSDKFCYEKLTBETEGKNGCGDGRMIOCSKHDFVCGFL 660  
 601 NGECKTRDNOCQYIWTGKAAGSDKFCYEKLTBETEGKNGCGDGRMIOCSKHDFVCGFL 660  
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 661 LCTNLTRAPRIIGOLOGEITPTSFYHOGRAVIDCSGAHVVLDDDDTVGVEDGTPCGPSMNC 720  
 661 LCTNLTRAPRIIGOLOGEITPTSFYHOGRAVIDCSGAHVVLDDDDTVGVEDGTPCGPSMNC 720  
 721 LDRKCLQIOALNMSSCPLDSKGVCSGHGVCSENEATCICDFTWAGTDCSIRDPVRNLHP 780  
 721 LDRKCLQIOALNMSSCPLDSKGVCSGHGVCSENEATCICDFTWAGTDCSIRDPVRNLHP 780  
 721 LDRKCLQIOALNMSSCPLDSKGVCSGHGVCSENEATCICDFTWAGTDCSIRDPVRNLHP 780  
 781 KDEGKRGASATNLIGSAGAILVAIYLGCTGGMCFKNVKKRRFPDTPGCGPI 832  
 781 KDEGKRGASATNLIGSAGAILVAIYLGCTGGMCFKNVKKRRFPDTPGCGPI 832  
 781 KDEGKRGASATNLIGSAGAILVAIYLGCTGGMCFKNVKKRRFPDTPGCGPI 832

US-10-202-675-4  
 Sequence 4, Application us/10202675  
 GENERAL INFORMATION:  
 APPLICANT: Cerretti, Douglas P.  
 TITLE OF INVENTION: SVPH3-13 AND SVPH3-17 DNA AND POLYPEPTIDES  
 FILE REFERENCE: 03260,0051-00304  
 CURRENT APPLICATION NUMBER: US/10/202,675  
 CURRENT FILING DATE: 2002-07-23  
 PRIOR APPLICATION NUMBER: US/09/634,252  
 PRIOR FILING DATE: 2000-08-07  
 PRIOR APPLICATION NUMBER: 60/074,310  
 PRIOR FILING DATE: 1998-02-11  
 NUMBER OF SEQ ID NOS: 10  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 4  
 LENGTH: 832  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-202-675-4

Query Match 100.0%; Score 4553; DB 26; Length 832;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 832; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKPPSSSRPPPLAGCSLAGASCGPORGAGSVASAPARTPPCRLLVLLPPLAAS 60  
 1 MKPPSSSRPPPLAGCSLAGASCGPORGAGSVASAPARTPPCRLLVLLPPLAAS 60  
 61 RPRAGAAAPAPAHNETAEKRLGVLADENLTLOONSSNISYSNAMOKEITLPSRLIY 120  
 61 RPRAGAAAPAPAHNETAEKRLGVLADENLTLOONSSNISYSNAMOKEITLPSRLIY 120  
 61 RPRAGAAAPAPAHNETAEKRLGVLADENLTLOONSSNISYSNAMOKEITLPSRLIY 120  
 121 INODESEYHVLDTKARHQQHKAHVAHQAQSFQIEAFGSKFLDLINNGLLSPYVEI 180  
 121 INODESEYHVLDTKARHQQHKAHVAHQAQSFQIEAFGSKFLDLINNGLLSPYVEI 180  
 121 INODESEYHVLDTKARHQQHKAHVAHQAQSFQIEAFGSKFLDLINNGLLSPYVEI 180  
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 241 KSTGRPHIIOKTLAAGYSKOMKNTLMERGDOMPLSELQWLKRRKRAVNSRGIFEEMKY 300  
 241 KSTGRPHIIOKTLAAGYSKOMKNTLMERGDOMPLSELQWLKRRKRAVNSRGIFEEMKY 300  
 241 KSTGRPHIIOKTLAAGYSKOMKNTLMERGDOMPLSELQWLKRRKRAVNSRGIFEEMKY 300  
 301 LELMIVNDHKTYYKRRSSHAHTNFAKSVNLVDSIYKEQLNTRVVAVEETWTEKDOID 360  
 301 LELMIVNDHKTYYKRRSSHAHTNFAKSVNLVDSIYKEQLNTRVVAVEETWTEKDOID 360  
 301 LELMIVNDHKTYYKRRSSHAHTNFAKSVNLVDSIYKEQLNTRVVAVEETWTEKDOID 360  
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 361 ITTNPVQMLHFSKYRORIKOHADAVHLISRVTFFHYKRSLSYFGVGCRTGAVNEYG 420  
 361 ITTNPVQMLHFSKYRORIKOHADAVHLISRVTFFHYKRSLSYFGVGCRTGAVNEYG 420  
 421 LPMVAQVLSQSLAONLGIOWEPSSRRPKDCDCTESMGCCIMEETGVSHSRKFSKSILEY 480  
 421 LPMVAQVLSQSLAONLGIOWEPSSRRPKDCDCTESMGCCIMEETGVSHSRKFSKSILEY 480  
 421 LPMVAQVLSQSLAONLGIOWEPSSRRPKDCDCTESMGCCIMEETGVSHSRKFSKSILEY 480  
 481 RDLFLOGGGACLFNRPKLEPTEECGNGYVEAGEECDCGFHVECYGLCKKCSLSNGAHC 540  
 481 RDLFLOGGGACLFNRPKLEPTEECGNGYVEAGEECDCGFHVECYGLCKKCSLSNGAHC 540  
 481 RDLFLOGGGACLFNRPKLEPTEECGNGYVEAGEECDCGFHVECYGLCKKCSLSNGAHC 540  
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 541 SDGPCCNTSCLFOPRGYECRDVAVNECDITEYCTGDSGCPNHLKHODGYACNOGRCY 600  
 541 SDGPCCNTSCLFOPRGYECRDVAVNECDITEYCTGDSGCPNHLKHODGYACNOGRCY 600  
 601 NGECKTRDNOCQYIWTGKAAGSDKFCYEKLTBETEGKNGCGDGRMIOCSKHDFVCGFL 660  
 601 NGECKTRDNOCQYIWTGKAAGSDKFCYEKLTBETEGKNGCGDGRMIOCSKHDFVCGFL 660  
 601 NGECKTRDNOCQYIWTGKAAGSDKFCYEKLTBETEGKNGCGDGRMIOCSKHDFVCGFL 660  
 661 LCTNLTRAPRIIGOLOGEITPTSFYHOGRAVIDCSGAHVVLDDDDTVGVEDGTPCGPSMNC 720  
 661 LCTNLTRAPRIIGOLOGEITPTSFYHOGRAVIDCSGAHVVLDDDDTVGVEDGTPCGPSMNC 720  
 661 LCTNLTRAPRIIGOLOGEITPTSFYHOGRAVIDCSGAHVVLDDDDTVGVEDGTPCGPSMNC 720  
 721 LDRKCLQIOALNMSSCPLDSKGVCSGHGVCSENEATCICDFTWAGTDCSIRDPVRNLHP 780  
 721 LDRKCLQIOALNMSSCPLDSKGVCSGHGVCSENEATCICDFTWAGTDCSIRDPVRNLHP 780  
 721 LDRKCLQIOALNMSSCPLDSKGVCSGHGVCSENEATCICDFTWAGTDCSIRDPVRNLHP 780

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Db      721 LDRKLOIALNMSSCPLDSKGVCSGHCNSNATCICDPTWAGTDCSTIRDPVRLNHP 780
QY      761 KDEGPKGSATNLIGSTAGAILVAALVIGTGCGFKFNKKRRPDPDQGP 832
Db      761 KDEGPKGSATNLIGSTAGAILVAALVIGTGCGFKFNKKRRPDPDQGP 832

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## RESULT 5

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US-09-791-537-142799
: Sequence 142799, Application US/09791537
: GENERAL INFORMATION:
: APPLICANT: Biocomix, Inc.
: APPLICANT: Debe, Derek
: APPLICANT: Danzer, Joseph
: TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
: TITLE OF INVENTION: METHODS OF USE THEREOF
: FILE REFERENCE: 261/210
: CURRENT APPLICATION NUMBER: US/09/791,537
: CURRENT FILING DATE: 2001-02-22
: NUMBER OF SEQ ID NOS: 153055
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 142799
: LENGTH: 829
: TYPE: PRT
: ORGANISM: Mus musculus
US-09-791-537-142799

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Query Match      93.6%; Score 4239.5; DB 21; Length 829;
Best Local Similarity 93.8%; Pred. No. 0;
Matches 781; Conservative 16; Mismatches 31; Indels 5; Gaps 2;

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QY      1 MKPSSSSRPPPLACSLAGACGQGRGAPASAPAPAPRPPRLVLLPLLAASS 60
Db      1 MKPSSISRPPPLTGCSLPGASCGRCPAPV-----PARAPCRLVLLVLLPALATSS 56
QY      61 PRAGCAAPAPAPHNETAEKNLGVLADEDNLTQONSS- NISYSNAOKEITLPSRLIY 119
Db      57 PRAGCAAPAPAPHNETAEKNLGVLADEDNLTQONSSNRTSYSAVOKEITLPSRLIY 116
QY      120 YINDSESPYHVLDTKARHQQHNKAVHLAQSFOIAFGSKFTLDLILNGLSSDYVE 179
Db      117 YINDSESPYHVLDTKARHQQHNKAVHLAQSFOIAFGSKFTLDLILNGLSSDYVE 176
QY      180 IYENGKPOYSKGEHCYHGSIRGVDSKVALSTCGLHGMFEDDTFYVMIPELVD 239
Db      177 IYHEDGOMTSKGEHCYHGSIRGVDSKVALSTCGLHGMFEDDTFYVMIPELVD 236
QY      240 EKSTGRPHIIOKTLAGQYSKOMNLTMERGDQMPLELQWLKRRRAVNPSSRGIFEEMK 299
Db      237 EKSTGRPHIIOKTLAGQYSKOMNLTSDGSDQMPLELQWLKRRRAVNPSSRGIFEEMK 296
QY      300 YLELMTVNDHKTKYKRRSSHAHTNFAKSVNLVDSIYKEQLNTRVVLVAVETWTEKDI 359
Db      297 YLELMTVNDHKTKYKRRSSHAHTNFAKSVNLVDSIYKEQLNTRVVLVAVETWTEKDI 356
QY      360 DITTNPVOMLHEFSKYRORIKOHADA VHLISRVTFYKRRSSLSYGGVCSRTRGVNEY 419
Db      357 DITTNPVOMLHEFSKYRORIKOHADA VHLISRVTFYKRRSSLSYGGVCSRTRGVNEY 416
QY      420 GLPMAVAOVLSSLOANLGIOWEPSSRRKPCDCTESWGCIMEETGVSHSRKFSKCSLLE 479
Db      417 GLPMAVAOVLSSLOANLGIOWEPSSRRKPCDCTESWGCIMEETGVSHSRKFSKCSLLE 476
QY      480 YRDFLORGGACLFNRP TKLFPEPTCGNGYVAGEECDCGPHVCEYGCCKKCSLSNGAH 539
Db      477 YRDFLORGGACLFNRP TKLFPEPTCGNGYVAGEECDCGPHVCEYGCCKKCSLSNGAH 536
QY      540 GSDGCCNNTSCLTROPGRYECRDVANECDITEYCTGDSGQCPPLHLHODGYACQONGRC 599
Db      537 GSDGCCNNTSCLTROPGRYECRDVANECDITEYCTGDSGQCPPLHLHODGYACQONGRC 596
QY      600 YNGEKTBDNOCQYIMGTAKAGSDKFCYEKLTNETGTEKNGCKGDRWIOCSKHDFVCGF 659

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Db      597 YNGEKTBDNOCQYIMGTAKAGSDKFCYEKLTNETGTEKNGCKGDRWIOCSKHDFVCGF 656
QY      660 LICTNITRAPRIGOLGELIPIPSFYHOGRVIDCSGAHVLDLDDPDYGVEDGTGCGFSM 719
Db      657 LICTNITRAPRIGOLGELIPIPSFYHOGRVIDCSGAHVLDLDDPDYGVEDGTGCGFSM 716
QY      720 CLDRKLOIALNMSSCPLDSKGVCSGHCNSNATCICDPTWAGTDCSTIRDPVRLNHP 779
Db      717 CLDRKLOIALNMSSCPLDSKGVCSGHCNSNATCICDPTWAGTDCSTIRDPVRLNHP 776
QY      780 KDEGPKGSATNLIGSTAGAILVAALVIGTGCGFKFNKKRRPDPDQGP 832
Db      777 KDEGPKGSATNLIGSTAGAILVAALVIGTGCGFKFNKKRRPDPDQGP 829

```

## RESULT 6

```

US-09-760-484-315
: Sequence 315, Application US/09760484
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PTA3
: CURRENT APPLICATION NUMBER: US/09/760,484
: CURRENT FILING DATE: 2001-01-16
: Prior application data removed - consult PALM or file wrapper
: NUMBER OF SEQ ID NOS: 638
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 315
: LENGTH: 776
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (731)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-760-484-315

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Query Match      91.9%; Score 4186; DB 21; Length 776;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 759; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

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QY      57 AASSRPRAMGAAPAPHNETAEKNLGVLADEDNLTQONSSNISYSNAOKEITLPSR 116
Db      1 AASSRPRAMGAAPAPHNETAEKNLGVLADEDNLTQONSSNISYSNAOKEITLPSR 60
QY      117 LIYINODSESPYHVLDTKARHQQHNKAVHLAQSFOIAFGSKFTLDLILNGLSSD 176
Db      61 LIYINODSESPYHVLDTKARHQQHNKAVHLAQSFOIAFGSKFTLDLILNGLSSD 120
QY      177 YVEIHYENGKPOYSKGEHCYHGSIRGVDSKVALSTCGLHGMFEDDTFYVMIPEL 236
Db      121 YVEIHYENGKPOYSKGEHCYHGSIRGVDSKVALSTCGLHGMFEDDTFYVMIPEL 180
QY      237 VHDKSTGRPHIIOKTLAGQYSKOMNLTMERGDQMPLELQWLKRRRAVNPSSRGIFE 296
Db      181 VHDKSTGRPHIIOKTLAGQYSKOMNLTMERGDQMPLELQWLKRRRAVNPSSRGIFE 240
QY      297 EMKYLELMTVNDHKTKYKRRSSHAHTNFAKSVNLVDSIYKEQLNTRVVLVAVETWTEK 356
Db      241 EMKYLELMTVNDHKTKYKRRSSHAHTNFAKSVNLVDSIYKEQLNTRVVLVAVETWTEK 300
QY      357 DQDITTNPVOMLHEFSKYRORIKOHADA VHLISRVTFYKRRSSLSYGGVCSRTRGV 416
Db      301 DQDITTNPVOMLHEFSKYRORIKOHADA VHLISRVTFYKRRSSLSYGGVCSRTRGV 360
QY      417 NEYGLPMAVAOVLSSLOANLGIOWEPSSRRKPCDCTESWGCIMEETGVSHSRKFSKCS 476
Db      361 NEYGLPMAVAOVLSSLOANLGIOWEPSSRRKPCDCTESWGCIMEETGVSHSRKFSKCS 420
QY      477 ILEYRDFLORGGACLFNRP TKLFPEPTCGNGYVAGEECDCGPHVCEYGCCKKCSLSN 536
Db      421 ILEYRDFLORGGACLFNRP TKLFPEPTCGNGYVAGEECDCGPHVCEYGCCKKCSLSN 480

```



Qy	537	GAHSDSPCCNNITSGLEFPGREYECADANNECOTITECTSDSQC PNLLHKODYACIHOQ	596
Db	481	GAHSDSPCCNNITSGLEFPGREYECADANNECOTITECTSDSQC PNLLHKODYACIHOQ	540
Qy	597	GRCYNGECKTRDNOCOYIWTGKAAGSDKFCYEKLTBEGTEKNGCKGDRMTDCKSHDYF	656
Db	541	GRCYNGECKTRDNOCOYIWTGKAAGSDKFCYEKLTBEGTEKNGCKGDRMTDCKSHDYF	600
Qy	657	CGFLCTNLTRAPRIGOLOGETIPTSPFHOGVIDCSGAHVYLLDDPTDVGVEDEGRJCGP	716
Db	601	CGFLCTNLTRAPRIGOLOGETIPTSPFHOGVIDCSGAHVYLLDDPTDVGVEDEGRJCGP	660
Qy	717	SMMLCDRKCIOIALNMSSCPIDSKGKVCSGHGYCSNEATYCICTDFTWAGTDCSIRDPVRN	776
Db	661	SMMLCDRKCIOIALNMSSCPIDSKGKVCSGHGYCSNEATYCICTDFTWAGTDCSIRDPVRN	720
Qy	777	LHPKIDGPGKSPATNLITGSIAGILLVAAYLGITGKCFKVVKKRRRPTDQGP	832
Db	721	LHPKIDGPGKSPATNLITGSIAGILLVAAYLGITGKCFKVVKKRRRPTDQGP	775

```

RESULT 7
US-09-631-534-10
; Sequence 10. Application US/09631534
;
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Balindur, Nand
; APPLICANT: Delshter, Theresa A.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Taft, David W.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOGUE, MAHBP
; FILE REFERENCE: 98-29C1
; CURRENT APPLICATION NUMBER: US/09/631,534
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/092,371
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/147, 410
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 709
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-631-534-10

```

Query Match	84.6%	Score 3851	DB 20	Length 709
Best Local Similarity	99.7%	Pred. No. 4.7e-301		
Matches 699	Conservative 0	Mismatches 2	Indels 0	5aps 0

Qy	132	LDTKARHQKNNKAVHLAQASFOJAEFQSKFLTDLILNGLSSDVEYELHENGKQOYK	191
Db	9	LDTKARHQKNNKAVHLAQASFOJAEFQSKFLTDLILNGLSSDVEYELHENGKQOYK	68
Qy	192	GGECYTHGSTRGVKDSKVYALSTCGLHGMFEDDPVYVIEPRLVHDEKSTGRPIIOK	251
Db	69	GGECYVHGSTRGVKDSKVYALSTCGLHGMFEDDPVYVIEPRLVHDEKSTGRPIIOK	128
Qy	252	TLAGQYKQKNNLTMERGDQMPFLSELQMLKRRKRAVNPNSRGIIEEMKLTLEIMTVNDHKT	311
Db	129	TLAGQYKQKNNLTMERGDQMPFLSELQMLKRRKRAVNPNSRGIIEEMKLTLEIMTVNDHKT	188
Qy	312	YKRRSSHHTNNFAKSVYLVDSITYKEQLNTRVYLAVEYTEMKQDIDITTPVOYMLHE	371
Db	189	YKRRSSHHTNNFAKSVYLVDSITYKEQLNTRVYLAVEYTEMKQDIDITTPVOYMLHE	248
Qy	372	FSKTRORIKQADAVHLISRYTFPHKRSLSLTFEGVCSTRTGVNVEYGLPMAVAVOYLSQ	431
Db	249	FSKTRORIKQADAVHLISRYTFPHKRSLSLTFEGVCSTRTGVNVEYGLPMAVAVOYLSQ	308

QY	432	SLAONLGIOMPESSSKPKCDCTESMGGCIMETGVSHSKFSKCSLLEYRDFLORGGGAC	491
Dd	309	SLAONLGIOMPESSSKPKCDCTESMGGCIMETGVSHSKFSKCSLLEYRDFLORGGGAC	368
QY	492	LENRPYTKLEPTECGNGVYEAGEECCDGFHVECYGLCKKCSLSNGAHCSDBGCCNNTSC	551
Dd	369	LENRPYTKLEPTECGNGVYEAGEECCDGFHVECYGLCKKCSLSNGAHCSDBGCCNNTSC	428
QY	552	LFOPRGYECRDVAVNECDITTEYCTGDSGOCPPMLHKODGYACACNONOGRCTNGECKTRDNOC	611
Dd	429	LFOPRGYECRDVAVNECDITTEYCTGDSGOCPPMLHKODGYACACNONOGRCTNGECKTRDNOC	488
QY	612	OYIMWTKAAGSNPKFCEYKLNTEGTEBKNGCKGKDRMIOCSKHDPVFGFLICTNLUTRAPRI	671
Dd	489	OYIMWTKAAGSNPKFCEYKLNTEGTEBKNGCKGKDRMIOCSKHDPVFGFLICTNLUTRAPRI	548
QY	672	GOLGGEIIPTESEYHOGRAVYDCSGAHVYLDDDPDVGYVEEGTGPCGSPMMCILDRKCLIOAL	731
Dd	549	GOLGGEIIPTESEYHOGRAVYDCSGAHVYLDDDPDVGYVEEGTGPCGSPMMCILDRKCLIOAL	608
QY	732	NMSSCPUDSKGKVCSGHGVCNSNEATPCIDPFTNAGTDCSIRDPVRLNLHPKDEGPKGPSAT	791
Dd	609	NMSSCPUDSKGKVCSGHGVCNSNEATPCIDPFTNAGTDCSIRDPVRLNLHPKDEGPKGPSAT	668
QY	792	NLITGSITGAILVAIVAILVGTGTGMRNVKRRRPFDPQOGPI	832
Dd	669	NLITGSITGAILVAIVAILVGTGTGMRNVKRRRPFDPQOGPI	709

```

RESULT 8
US-10-260-506-10
: Sequence 10, Application US/10260506
: GENERAL INFORMATION:
: APPLICANT: Sheppard, Paul O.
: APPLICANT: Baindur, Nand
: APPLICANT: Deishner, Theresa A.
: APPLICANT: Bishop, Paul D.
: APPLICANT: Taft, David W.
: TITLE OF INVENTION: DISINTEGRIN HOMOLOGUE, MAHBP
: FILE REFERENCE: 98-29c1
: CURRENT APPLICATION NUMBER: US/10/260,506
: CURRENT FILING DATE: 2002-09-27
: PRIOR APPLICATION NUMBER: 60/092,371
: PRIOR FILING DATE: 1998-07-10
: PRIOR APPLICATION NUMBER: 60/147, 410
: PRIOR FILING DATE: 1999-08-05
: PRIOR APPLICATION NUMBER: 09/351,414
: PRIOR FILING DATE: 1999-07-09
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 10
: LENGTH: 709
: TYPE: prt
: ORGANISM: Homo sapiens
US-10-260-506-10

```

Query Match	84.68;	Score 3851;	DB 26;	Length 709;
Best Local Similarity	99.78;	Pred. No. 4.7e-301;		
Matches 699;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0

[illegible]

```
Db 189 YKKHRSHTNNFAKSVNLVDSYKEQJLNTRVVLAVETWEKDOIITLTNPVOMLHE 248
QY 372 FSKYRORIKQAHADAVHLISRVTFRHKRSSLSYFGVCSRTRGVAVNEGLPMAVAQVLSQ 431
Db 249 FSKYRORIKQAHADAVHLISRVTFRHKRSSLSYFGVCSRTRGVAVNEGLPMAVAQVLSQ 308
QY 432 SLAONIGIOWEPSSRRPKCDCTESWGCIIMEETGVSHSRFSKCSLLEYRDLQRCGGAC 491
Db 309 SLAONIGIOWEPSSRRPKCDCTESWGCIIMEETGVSHSRFSKCSLLEYRDLQRCGGAC 368
QY 492 LFNRPRTKLEPTEGNGYVEAGEECDCGFHVECYGLCCCKCSLSNGAHCSDGPCNNNTSC 551
Db 369 LFNRPRTKLEPTEGNGYVEAGEECDCGFHVECYGLCCCKCSLSNGAHCSDGPCNNNTSC 428
QY 552 LFNRPRTKLEPTEGNGYVEAGEECDCGFHVECYGLCCCKCSLSNGAHCSDGPCNNNTSC 611
Db 429 LFNRPRTKLEPTEGNGYVEAGEECDCGFHVECYGLCCCKCSLSNGAHCSDGPCNNNTSC 488
QY 612 OYIWTGTRKAAGSDKFCYEKLTNTEGTEKNGCGKDGDRWIQCSKHDFVCGFLCTNLTRAPRI 671
Db 489 OYIWTGTRKAAGSDKFCYEKLTNTEGTEKNGCGKDGDRWIQCSKHDFVCGFLCTNLTRAPRI 548
QY 672 GOLGELIIPSTFYHOGRAVIDCSGAHVLDLDDTVGVYEDTGPCPSMCLDRKCLQIOL 731
Db 549 GOLGELIIPSTFYHOGRAVIDCSGAHVLDLDDTVGVYEDTGPCPSMCLDRKCLQIOL 608
QY 732 NMSSCPDLSKRGKVCSGHGVCSNEATCICDFTWAGTDCSIRDPVRNLHPKDEGPKGPAT 791
Db 609 NMSSCPDLSKRGKVCSGHGVCSNEATCICDFTWAGTDCSIRDPVRNLHPKDEGPKGPAT 668
QY 792 NLIISGAILIYVAIYVGGTGMFKNKRRFEDTQOGPI 832
Db 669 NLIISGAILIYVAIYVGGTGMFKNKRRFEDTQOGPI 709

RESULT 9
US-09-631-534-2
: Sequence 2, Application US/09631534
: GENERAL INFORMATION:
: APPLICANT: Sheppard, Paul O.
: APPLICANT: Baidur, Nand
: APPLICANT: Delsher, Theresa A.
: APPLICANT: Bishop, Paul D.
: APPLICANT: Tait, David W.
: TITLE OF INVENTION: DISINTEGRIN HOMOLOGUE, MAHBP
: FILE REFERENCE: 98-29C1
: CURRENT APPLICATION NUMBER: US/09/631,534
: PRIOR APPLICATION NUMBER: 2000-08-03
: PRIOR FILING DATE: 1998-07-10
: PRIOR FILING DATE: 1999-08-05
: PRIOR APPLICATION NUMBER: 09/351,414
: PRIOR FILING DATE: 1999-07-09
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 696
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-631-534-2

Query Match 79.5%; Score 3621; DB 20; Length 696;
Best Local Similarity 99.7%; Pred. No. 1.7e-282;
Matches 654; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 132 LDTKARHQQKHNKAVHLAASFOIEAFGSKFTLIDLINGLSSDYVEIHYENGRPOYSK 191
Db 9 LDTKARHQQKHNKAVHLAASFOIEAFGSKFTLIDLINGLSSDYVEIHYENGRPOYSK 68
QY 192 GGEHCYHGSIRGVKDSKVALSTCNGLHGMFEDDTFYVMIPELTVHDEKSTGRPHIIOK 251
Db 192 GGEHCYHGSIRGVKDSKVALSTCNGLHGMFEDDTFYVMIPELTVHDEKSTGRPHIIOK 251
```

```
Db 69 GGEHCYHGSIRGVKDSKVALSTCNGLHGMFEDDTFYVMIPELTVHDEKSTGRPHIIOK 128
QY 252 TLAGOSKRMKMLTHERGOMPFLELQWLKRRRAVNSRQIFEMKYLELMTVNDHKT 311
Db 129 TLAGOSKRMKMLTHERGOMPFLELQWLKRRRAVNSRQIFEMKYLELMTVNDHKT 188
QY 312 YKKHRSHTNNFAKSVNLVDSYKEQJLNTRVVLAVETWEKDOIITLTNPVOMLHE 371
Db 189 YKKHRSHTNNFAKSVNLVDSYKEQJLNTRVVLAVETWEKDOIITLTNPVOMLHE 248
QY 372 FSKYRORIKQAHADAVHLISRVTFRHKRSSLSYFGVCSRTRGVAVNEGLPMAVAQVLSQ 431
Db 249 FSKYRORIKQAHADAVHLISRVTFRHKRSSLSYFGVCSRTRGVAVNEGLPMAVAQVLSQ 308
QY 432 SLAONIGIOWEPSSRRPKCDCTESWGCIIMEETGVSHSRFSKCSLLEYRDLQRCGGAC 491
Db 309 SLAONIGIOWEPSSRRPKCDCTESWGCIIMEETGVSHSRFSKCSLLEYRDLQRCGGAC 368
QY 492 LFNRPRTKLEPTEGNGYVEAGEECDCGFHVECYGLCCCKCSLSNGAHCSDGPCNNNTSC 551
Db 369 LFNRPRTKLEPTEGNGYVEAGEECDCGFHVECYGLCCCKCSLSNGAHCSDGPCNNNTSC 428
QY 552 LFNRPRTKLEPTEGNGYVEAGEECDCGFHVECYGLCCCKCSLSNGAHCSDGPCNNNTSC 611
Db 429 LFNRPRTKLEPTEGNGYVEAGEECDCGFHVECYGLCCCKCSLSNGAHCSDGPCNNNTSC 488
QY 612 OYIWTGTRKAAGSDKFCYEKLTNTEGTEKNGCGKDGDRWIQCSKHDFVCGFLCTNLTRAPRI 671
Db 489 OYIWTGTRKAAGSDKFCYEKLTNTEGTEKNGCGKDGDRWIQCSKHDFVCGFLCTNLTRAPRI 548
QY 672 GOLGELIIPSTFYHOGRAVIDCSGAHVLDLDDTVGVYEDTGPCPSMCLDRKCLQIOL 731
Db 549 GOLGELIIPSTFYHOGRAVIDCSGAHVLDLDDTVGVYEDTGPCPSMCLDRKCLQIOL 608
QY 732 NMSSCPDLSKRGKVCSGHGVCSNEATCICDFTWAGTDCSIRDPVRNLHPKDEGPKGPAT 791
Db 609 NMSSCPDLSKRGKVCSGHGVCSNEATCICDFTWAGTDCSIRDPVRNLHPKDEGPKGPAT 664

RESULT 10
US-09-809-617-2
: Sequence 2, Application US/09809617
: GENERAL INFORMATION:
: APPLICANT: Sheppard, Paul O.
: APPLICANT: Baidur, Nand
: APPLICANT: Delsher, Theresa A.
: APPLICANT: Bishop, Paul D.
: TITLE OF INVENTION: DISINTEGRIN HOMOLOG
: FILE REFERENCE: 98-29
: CURRENT APPLICATION NUMBER: US/09/809,617
: PRIOR FILING DATE: 2001-03-15
: PRIOR APPLICATION NUMBER: US/09/351,414
: PRIOR FILING DATE: 1999-07-09
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 696
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-809-617-2

Query Match 79.5%; Score 3621; DB 22; Length 696;
Best Local Similarity 99.7%; Pred. No. 1.7e-282;
Matches 654; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 132 LDTKARHQQKHNKAVHLAASFOIEAFGSKFTLIDLINGLSSDYVEIHYENGRPOYSK 191
Db 9 LDTKARHQQKHNKAVHLAASFOIEAFGSKFTLIDLINGLSSDYVEIHYENGRPOYSK 68
QY 192 GGEHCYHGSIRGVKDSKVALSTCNGLHGMFEDDTFYVMIPELTVHDEKSTGRPHIIOK 251
Db 69 GGEHCYHGSIRGVKDSKVALSTCNGLHGMFEDDTFYVMIPELTVHDEKSTGRPHIIOK 128
```

```
OY 252 TLGAQYSKOMKMLTMRGDMPLSELQMLKRRRAVNSRGIPEEMKYLELMINDAKT 311
DB 129 TLGAQYSKOMKMLTMRGDMPLSELQMLKRRRAVNSRGIPEEMKYLELMINDAKT 188
OY 312 YKRRSSHAHTNNFAKSVNLVDSIYKQOLNTRVLA VETWEKDOI DITTPVQMLHE 371
DB 189 YKRRSSHAHTNNFAKSVNLVDSIYKQOLNTRVLA VETWEKDOI DITTPVQMLHE 248
OY 372 FSKYRRIKOHADAVHLISRVTFFHKKRSSLSYFGVCSRTRGVNGEGLPMAVAQVLSQ 431
DB 249 FSKYRRIKOHADAVHLISRVTFFHKKRSSLSYFGVCSRTRGVNGEGLPMAVAQVLSQ 308
OY 432 SLAONLGIOWEPSSRKPCKDCTESWGCI MEETGVSHSRKFSKCSILEYRDFLQRGGAC 491
DB 309 SLAONLGIOWEPSSRKPCKDCTESWGCI MEETGVSHSRKFSKCSILEYRDFLQRGGAC 368
OY 492 LFNRPRTKLEPTCEGNGVYVAGEECDCGFHVECYGLCKCKCSLSNGAHCSDGPCNNNTSC 551
DB 369 LFNRPRTKLEPTCEGNGVYVAGEECDCGFHVECYGLCKCKCSLSNGAHCSDGPCNNNTSC 428
OY 552 LFPGRGYECRDVAVNECDITEYCTGDSGQCPNHLHKQDGYACNONOGRVNGECKTRDNOC 611
DB 429 LFPGRGYECRDVAVNECDITEYCTGDSGQCPNHLHKQDGYACNONOGRVNGECKTRDNOC 488
OY 612 QYIMGTAKAGSDKFCYEKLTBETGKNGCKDGRWIOCSKHDFVCGFLCTNLTRAPRI 671
DB 489 QYIMGTAKAGSDKFCYEKLTBETGKNGCKDGRWIOCSKHDFVCGFLCTNLTRAPRI 548
OY 672 GOLGELIPTSFYHOGRVIDCSGAHVVLDDPTDVGVEDETPCGSPMMLDRKCLQIOLAL 731
DB 549 GOLGELIPTSFYHOGRVIDCSGAHVVLDDPTDVGVEDETPCGSPMMLDRKCLQIOLAL 608
OY 732 NMSSCPLDSKGVCSGHGVCSEATCICDFTWAGTDCSIRDVPRNHLPPKDEGPKG 787
DB 609 NMSSCPLDSKGVCSGHGVCSEATCICDFTWAGTDCSIRDVPRNHLPPKDEGPKG 564
```

```
RESULT 11
US-09-809-790-2
: Sequence 2, Application US/09809790
: GENERAL INFORMATION:
: APPLICANT: Sheppard, Paul O.
: APPLICANT: Balindur, Nand
: APPLICANT: Deisher, Theresa A.
: APPLICANT: Bishop, Paul D.
: TITLE OF INVENTION: DISINTEGRIN HOMOLOG
: FILE REFERENCE: 98-29
: CURRENT APPLICATION NUMBER: US/09/809,790
: CURRENT FILING DATE: 2001-03-16
: PRIOR APPLICATION NUMBER: 09/351,414
: PRIOR FILING DATE: 1999-07-09
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 696
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-809-790-2
```

```
Query Match 79.5%: Score 3621; DB 22: Length 696;
Best Local Similarity 99.7%: Pred. No. 1.7e-282;
Matches 654: Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 132 LDTKARHOQKHNKAVHLAQAQSFQIEAFGSKFIDLILNGLSSDYVEIHYENKPOYSK 191
DB 9 LDTKARHOQKHNKAVHLAQAQSFQIEAFGSKFIDLILNGLSSDYVEIHYENKPOYSK 68
OY 192 GGEHCYHGSIRGVKDSKVALSTCNGLHGMFEDDTFVYMIPELVLHDEKSTGRPHITOK 251
DB 69 GGEHCYHGSIRGVKDSKVALSTCNGLHGMFEDDTFVYMIPELVLHDEKSTGRPHITOK 128
OY 252 TLGAQYSKOMKMLTMRGDMPLSELQMLKRRRAVNSRGIPEEMKYLELMINDAKT 311
DB 129 TLGAQYSKOMKMLTMRGDMPLSELQMLKRRRAVNSRGIPEEMKYLELMINDAKT 188
```

```
DB 129 TLGAQYSKOMKMLTMRGDMPLSELQMLKRRRAVNSRGIPEEMKYLELMINDAKT 188
OY 312 YKRRSSHAHTNNFAKSVNLVDSIYKQOLNTRVLA VETWEKDOI DITTPVQMLHE 371
DB 189 YKRRSSHAHTNNFAKSVNLVDSIYKQOLNTRVLA VETWEKDOI DITTPVQMLHE 248
OY 372 FSKYRRIKOHADAVHLISRVTFFHKKRSSLSYFGVCSRTRGVNGEGLPMAVAQVLSQ 431
DB 249 FSKYRRIKOHADAVHLISRVTFFHKKRSSLSYFGVCSRTRGVNGEGLPMAVAQVLSQ 308
OY 432 SLAONLGIOWEPSSRKPCKDCTESWGCI MEETGVSHSRKFSKCSILEYRDFLQRGGAC 491
DB 309 SLAONLGIOWEPSSRKPCKDCTESWGCI MEETGVSHSRKFSKCSILEYRDFLQRGGAC 368
OY 492 LFNRPRTKLEPTCEGNGVYVAGEECDCGFHVECYGLCKCKCSLSNGAHCSDGPCNNNTSC 551
DB 369 LFNRPRTKLEPTCEGNGVYVAGEECDCGFHVECYGLCKCKCSLSNGAHCSDGPCNNNTSC 428
OY 552 LFPGRGYECRDVAVNECDITEYCTGDSGQCPNHLHKQDGYACNONOGRVNGECKTRDNOC 611
DB 429 LFPGRGYECRDVAVNECDITEYCTGDSGQCPNHLHKQDGYACNONOGRVNGECKTRDNOC 488
OY 612 QYIMGTAKAGSDKFCYEKLTBETGKNGCKDGRWIOCSKHDFVCGFLCTNLTRAPRI 671
DB 489 QYIMGTAKAGSDKFCYEKLTBETGKNGCKDGRWIOCSKHDFVCGFLCTNLTRAPRI 548
OY 672 GOLGELIPTSFYHOGRVIDCSGAHVVLDDPTDVGVEDETPCGSPMMLDRKCLQIOLAL 731
DB 549 GOLGELIPTSFYHOGRVIDCSGAHVVLDDPTDVGVEDETPCGSPMMLDRKCLQIOLAL 608
OY 732 NMSSCPLDSKGVCSGHGVCSEATCICDFTWAGTDCSIRDVPRNHLPPKDEGPKG 787
DB 609 NMSSCPLDSKGVCSGHGVCSEATCICDFTWAGTDCSIRDVPRNHLPPKDEGPKG 564
```

```
RESULT 12
US-10-260-506-2
: Sequence 2, Application US/10260506
: GENERAL INFORMATION:
: APPLICANT: Sheppard, Paul O.
: APPLICANT: Balindur, Nand
: APPLICANT: Deisher, Theresa A.
: APPLICANT: Taft, David W.
: TITLE OF INVENTION: DISINTEGRIN HOMOLOGUE, MAHBP
: FILE REFERENCE: 98-29C1
: CURRENT APPLICATION NUMBER: US/10/260,506
: CURRENT FILING DATE: 2002-09-27
: PRIOR APPLICATION NUMBER: 60/092,371
: PRIOR FILING DATE: 1998-07-10
: PRIOR APPLICATION NUMBER: 60/147,410
: PRIOR FILING DATE: 1999-08-05
: PRIOR APPLICATION NUMBER: 09/351,414
: PRIOR FILING DATE: 1999-07-09
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 696
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-260-506-2
```

```
Query Match 79.5%: Score 3621; DB 26: Length 696;
Best Local Similarity 99.7%: Pred. No. 1.7e-282;
Matches 654: Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 132 LDTKARHOQKHNKAVHLAQAQSFQIEAFGSKFIDLILNGLSSDYVEIHYENKPOYSK 191
DB 9 LDTKARHOQKHNKAVHLAQAQSFQIEAFGSKFIDLILNGLSSDYVEIHYENKPOYSK 68
OY 192 GGEHCYHGSIRGVKDSKVALSTCNGLHGMFEDDTFVYMIPELVLHDEKSTGRPHITOK 251
DB 69 GGEHCYHGSIRGVKDSKVALSTCNGLHGMFEDDTFVYMIPELVLHDEKSTGRPHITOK 128
```

QY 252 TLAGYYSKOMKMLTMRGDMPFLSELQWLKRRRAVNPSRGIFEEEMKYLELMIVNDHKT 311  
 |||||  
 Db 129 TLAGYYSKOMKMLTMRGDMPFLSELQWLKRRRAVNPSRGIFEEEMKYLELMIVNDHKT 188  
 |||||  
 QY 312 YKHHSSHAHTNNPAKSVNLVDSTYKEQLNTRVLAVETWTEKDQIDITTPVOMLHE 371  
 |||||  
 Db 189 YKHHSSHAHTNNPAKSVNLVDSTYKEQLNTRVLAVETWTEKDQIDITTPVOMLHE 248  
 |||||  
 QY 372 FSKYRORIKOHADAVHLISRVTFHKRSSLSYFEGVCSRTRGVNEGYGLPMAVAQVLSQ 431  
 |||||  
 Db 249 FSKYRORIKOHADAVHLISRVTFHKRSSLSYFEGVCSRTRGVNEGYGLPMAVAQVLSQ 308  
 |||||  
 QY 432 SLAONLGIOMEPSRRPKDCCTESMGCIMEETGVSHSRKFSKCSILEYRDFLORGGAC 491  
 |||||  
 Db 309 SLAONLGIOMEPSRRPKDCCTESMGCIMEETGVSHSRKFSKCSILEYRDFLORGGAC 368  
 |||||  
 QY 492 LFNRPTKLEPTECGNGVYEAEBECDGFFHVECYGLCKKCSLSNGAHCSDBGPCNNTSC 551  
 |||||  
 Db 369 LFNRPTKLEPTECGNGVYEAEBECDGFFHVECYGLCKKCSLSNGAHCSDBGPCNNTSC 428  
 |||||  
 QY 552 LFOPRGYECRDVNECDITEYCTGDSGQCPNLIHKODGYACNONOGRCTNGECKTRDNC 611  
 |||||  
 Db 429 LFOPRGYECRDVNECDITEYCTGDSGQCPNLIHKODGYACNONOGRCTNGECKTRDNC 488  
 |||||  
 QY 612 QYIMGTAKAGSDKFCYEKINTEGTEKNGCKDGRWIOCSKHDFCFGLCTNLTRAPRI 671  
 |||||  
 Db 489 QYIMGTAKAGSDKFCYEKINTEGTEKNGCKDGRWIOCSKHDFCFGLCTNLTRAPRI 548  
 |||||  
 QY 672 GOLGEEIIPTSFYHOGRVIDCSGAHVYLDLDDTDVGYVEDGTPCGPSMMCLDRKCIQIAL 731  
 |||||  
 Db 549 GOLGEEIIPTSFYHOGRVIDCSGAHVYLDLDDTDVGYVEDGTPCGPSMMCLDRKCIQIAL 608  
 |||||  
 QY 732 NMSSCPJDSKGVCSGHVCSNEATCICDFTWAGTDCSIRDPVRLHPPKDEGPKG 787  
 |||||  
 Db 609 NMSSCPJDSKGVCSGHVCSNEATCICDFTWAGTDCSIRDPVRLHPPKDEGPKG 664  
 |||||

Search completed: June 1, 2003, 18:48:56  
 Job time : 826 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 1, 2003, 18:17:26 ; Search time 197 Seconds  
(without alignments)  
874.976 Million cell updates/sec

Title: US-09-634-252A-4

Perfect score: 4553  
Sequence: 1 MKPPGSSSRPPPLAGCSLAG.....GMGFKNKRRPDPQGPPI 832

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 996614 seqs, 207175905 residues

Total number of hits satisfying chosen parameters: 996614

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Pending Patents AA New.\*  
1: /cgn2-6/ptodata/1/paa/PCU\_NEW\_COMB.pep.\*  
2: /cgn2-6/ptodata/1/paa/US06\_NEW\_COMB.pep.\*  
3: /cgn2-6/ptodata/1/paa/US07\_NEW\_COMB.pep.\*  
4: /cgn2-6/ptodata/1/paa/US08\_NEW\_COMB.pep.\*  
5: /cgn2-6/ptodata/1/paa/US09\_NEW\_COMB.pep.\*  
6: /cgn2-6/ptodata/1/paa/US10\_NEW\_COMB.pep.\*  
7: /cgn2-6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	4553	100.0	832	US-10-359-464-3	Sequence 3, App1
2	4553	100.0	832	US-10-126-052A-150	Sequence 150, App1
3	4553	100.0	832	US-10-126-052A-325	Sequence 325, App1
4	3669	80.6	886	US-09-949-016-11203	Sequence 11203, A
5	1985.5	43.6	870	US-09-724-676-80847	Sequence 80847, A
6	1985.5	43.6	870	US-09-724-676A-80847	Sequence 80847, A
7	1983.5	43.6	899	PCT-US03-04508-64	Sequence 64, App1
8	1983	43.6	775	US-60-453-135-13204	Sequence 13204, A
9	1983	43.6	775	US-60-453-050-13204	Sequence 13204, A
10	1976.5	43.4	772	US-09-949-016-7315	Sequence 7315, App
11	1976.5	43.4	772	US-09-949-016-7315	Sequence 7315, App
12	1976.5	43.4	772	US-09-949-016-7315	Sequence 7315, App
13	1976.5	43.4	772	US-09-949-016-7315	Sequence 7315, App
14	1967	43.2	769	US-09-949-016-9605	Sequence 9605, App
15	1967	43.2	769	US-09-949-016-9605	Sequence 9605, App
16	1967	43.2	769	US-09-949-016-9605	Sequence 9605, App
17	1967	43.2	769	US-09-949-016-9605	Sequence 9605, App
18	1412.5	31.0	623	US-60-453-050-13203	Sequence 13203, A
19	1412.5	31.0	623	US-60-453-050-13203	Sequence 13203, A
20	1217	26.7	561	US-09-724-676-80848	Sequence 80848, A
21	1217	26.7	561	US-09-724-676-80848	Sequence 80848, A
22	1007.5	22.1	918	US-10-274-639-18	Sequence 18, App1
23	1007.5	22.1	918	US-10-333-574-18	Sequence 18, App1
24	1007.5	22.1	918	US-10-405-027-3117	Sequence 3117, App
25	986.5	21.7	886	US-60-455-444-4404	Sequence 4404, App
26	986.5	21.7	886	US-60-455-241-4404	Sequence 4404, App

27	986.5	21.7	923	7	US-60-455-444-4403	Sequence 4403, App
28	986.5	21.7	923	7	US-60-465-241-4403	Sequence 4403, App
29	986.5	21.7	923	7	US-09-949-016-8262	Sequence 8262, App
30	986.5	21.7	968	5	US-09-949-016-11229	Sequence 11229, A
31	967	21.2	914	6	US-10-028-248A-83	Sequence 83, App1
32	967	21.2	914	6	US-10-107-782-83	Sequence 83, App1
33	966	21.2	909	1	PCT-US02-19297-78	Sequence 78, App1
34	966	21.2	909	1	PCT-US02-19592-80	Sequence 80, App1
35	966	21.2	909	6	US-10-126-052A-427	Sequence 427, App
36	964	21.2	909	1	PCT-US02-37431-2	Sequence 2, App1
37	964	21.2	909	5	US-09-949-016-6370	Sequence 6370, App
38	964	21.2	909	6	US-10-301-822-2	Sequence 2, App1
39	962.5	21.1	735	6	US-10-145-087A-74	Sequence 74, App1
40	962.5	21.1	735	6	US-10-145-031A-74	Sequence 74, App1
41	962.5	21.1	735	6	US-10-145-092A-74	Sequence 74, App1
42	962.5	21.1	735	6	US-10-162-522A-74	Sequence 74, App1
43	962.5	21.1	735	6	US-10-165-038A-74	Sequence 74, App1
44	962.5	21.1	735	6	US-10-165-353-74	Sequence 74, App1
45	962.5	21.1	735	6	US-10-170-481A-74	Sequence 74, App1

#### ALIGNMENTS

RESULT 1  
US-10-359-464-3  
Sequence 3, Application US/10359464  
GENERAL INFORMATION:  
APPLICANT: Lopez-Olin, Carlos  
APPLICANT: Miguel, Santiago Cal  
APPLICANT: Freije, Jose Maria Perez  
APPLICANT: Garcia, Jose Manuel Lopez  
APPLICANT: Bianchi, Albert Bernard  
APPLICANT: Trall, Pamela  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING INTEGRIN-MEDIATED  
FILE REFERENCE: D0015 DIV  
CURRENT APPLICATION NUMBER: US/10/359,464  
CURRENT FILING DATE: 2003-02-05  
PRIOR APPLICATION NUMBER: 09/824,129  
PRIOR FILING DATE: 2001-04-02  
PRIOR APPLICATION NUMBER: 60/194,164  
PRIOR FILING DATE: 2000-04-03  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 3  
LENGTH: 832  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-359-464-3  
Query Match 100.0%; Score 4553; DB 6; Length 832;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 832; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 MKPPGSSSRPPPLAGCSLAGSCGPORGPAGSPASAPARTPPCRLDVLVLLPPLAAS 60  
1 MKPPGSSSRPPPLAGCSLAGSCGPORGPAGSPASAPARTPPCRLDVLVLLPPLAAS 60  
61 RPPAMGAAPASAPAHMETAEKNLGLVLADEDTLQONSSNYSINAMOKETPLPSRLYY 120  
61 RPPAMGAAPASAPAHMETAEKNLGLVLADEDTLQONSSNYSINAMOKETPLPSRLYY 120  
121 INDSSSPYHVLDTKARHOKHMKAVLAQASFOIEAFSGKFTLDLTLNGLSSDVEI 180  
121 INDSSSPYHVLDTKARHOKHMKAVLAQASFOIEAFSGKFTLDLTLNGLSSDVEI 180  
181 HYENGRPOYSKSGEHCYHGSIRGVKDSKVALSTCNGLHGMFEDDTFVYMEPELVHDE 240  
181 HYENGRPOYSKSGEHCYHGSIRGVKDSKVALSTCNGLHGMFEDDTFVYMEPELVHDE 240  
241 KSTGRPHITOKTLAGOTSKOMKULTMERGQWPLSLDLWKRRRAVNDPSRGTFEEMKY 300  
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Db 241 KSTGRPHIIOKTLAAGYSKOMKNTLWERGDMWFLSELOMLKRRRAVNPSSGJFEEMKY 300
Qy 301 LELMIVNDHKTYKKRRSSHAHTNNFAKSVVNLVDSIYKEQLNTRVLAVALVETWTEKDID 360
Db 301 LELMIVNDHKTYKKRRSSHAHTNNFAKSVVNLVDSIYKEQLNTRVLAVALVETWTEKDID 360
Qy 361 ITTNPVQMLHEFSKYRORIKOHADAVHLISRYTFHYKRSLSYFGVCSRTGVCVNEYG 420
Db 361 ITTNPVQMLHEFSKYRORIKOHADAVHLISRYTFHYKRSLSYFGVCSRTGVCVNEYG 420
Qy 421 LPMVAOVAVLSQSLAONLGIOMEPSRRPKCDCTESWGGCIMEETGVSHSRKFSKCSILEY 480
Db 421 LPMVAOVAVLSQSLAONLGIOMEPSRRPKCDCTESWGGCIMEETGVSHSRKFSKCSILEY 480
Qy 481 RPLORGGACLFNRPRTKLFEPTECGNGVYEAEGECDCGFHVECYGLCKKCSLSNGAHC 540
Db 481 RPLORGGACLFNRPRTKLFEPTECGNGVYEAEGECDCGFHVECYGLCKKCSLSNGAHC 540
Qy 541 SDGPCNNNTSCLFOPRGYECRDVNECDITEYCTGDSGQCPNMLHODGYACNONOGRCY 600
Db 541 SDGPCNNNTSCLFOPRGYECRDVNECDITEYCTGDSGQCPNMLHODGYACNONOGRCY 600
Qy 601 NGECKTRDNOCQYIMGTAKGSDKFCYEKLTETEGENCGKGDWRMIQCSKHDFCGFL 660
Db 601 NGECKTRDNOCQYIMGTAKGSDKFCYEKLTETEGENCGKGDWRMIQCSKHDFCGFL 660
Qy 661 LCTNLTRAPRIGOLGELIPTSEYHOGRVIDCSGAHVLDLDDTVGYVEDEGTGCGPSMMC 720
Db 661 LCTNLTRAPRIGOLGELIPTSEYHOGRVIDCSGAHVLDLDDTVGYVEDEGTGCGPSMMC 720
Qy 721 LDRKCLIOALNMSSCPDLSKGYCSGHGVSNEATCICDTWAGTDCSIRDPVRNLHP 780
Db 721 LDRKCLIOALNMSSCPDLSKGYCSGHGVSNEATCICDTWAGTDCSIRDPVRNLHP 780
Qy 781 KDEGPKGSPATNLLIGSISAGAILVAAILVGGTGMGFKNVKRRRDPDPOQGP 832
Db 781 KDEGPKGSPATNLLIGSISAGAILVAAILVGGTGMGFKNVKRRRDPDPOQGP 832

RESULT 2
US-10-126-052A-150
: Sequence 150, Application US/10126052A
: GENERAL INFORMATION:
: APPLICANT: Murray, Richard
: APPLICANT: Aziz, Natasha
: TITLE OF INVENTION: Methods of Diagnosis of Lung Cancer, Compositions and
: FILE REFERENCE: 018501-001530US
: CURRENT FILING DATE: 2002-04-18
: PRIOR FILING DATE: 2002-04-18
: PRIOR APPLICATION NUMBER: US 60/284,770
: PRIOR FILING DATE: 2001-04-18
: PRIOR APPLICATION NUMBER: US 60/290,492
: PRIOR FILING DATE: 2001-05-10
: PRIOR APPLICATION NUMBER: US 60/339,245
: PRIOR FILING DATE: 2001-11-09
: PRIOR APPLICATION NUMBER: US 60/350,666
: PRIOR FILING DATE: 2001-11-13
: PRIOR APPLICATION NUMBER: US 60/334,370
: PRIOR FILING DATE: 2001-11-29
: PRIOR APPLICATION NUMBER: US 60/372,246
: PRIOR FILING DATE: 2002-04-12
: NUMBER OF SEQ ID NOS: 691
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 150
: LENGTH: 832
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-126-052A-150

Query Match 100.0%; Score 4553; DB 6; Length 832;
Best Local Similarity 100.0%; Pred. No. 0;

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Matches 832: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKPEGSSRRPPLACCSISAGSCGPRGRPASVASAPRPPCRLLVLLLPPLAAS 60
Db 1 MKPEGSSRRPPLACCSISAGSCGPRGRPASVASAPRPPCRLLVLLLPPLAAS 60
Qy 61 RPRWGAAPSPAHNTEAEKMLGVLADEDNLTQONSSNISYSNAMOKETLPSRLIY 120
Db 61 RPRWGAAPSPAHNTEAEKMLGVLADEDNLTQONSSNISYSNAMOKETLPSRLIY 120
Qy 121 INODESPYHVLDTKARHQQKHNKAHVLAQSFQIEAGSKFIDLLINNGLSSDYEI 180
Db 121 INODESPYHVLDTKARHQQKHNKAHVLAQSFQIEAGSKFIDLLINNGLSSDYEI 180
Qy 181 HYENKRPQYSKGGEHCYHGSTIRGYKDSVALSTCNGLHGMEDDTFYMIETPLVHDE 240
Db 181 HYENKRPQYSKGGEHCYHGSTIRGYKDSVALSTCNGLHGMEDDTFYMIETPLVHDE 240
Qy 241 KSTGRPHIIOKTLAAGYSKOMKNTLWERGDMWFLSELOMLKRRRAVNPSSGJFEEMKY 300
Db 241 KSTGRPHIIOKTLAAGYSKOMKNTLWERGDMWFLSELOMLKRRRAVNPSSGJFEEMKY 300
Qy 301 LELMIVNDHKTYKKRRSSHAHTNNFAKSVVNLVDSIYKEQLNTRVLAVALVETWTEKDID 360
Db 301 LELMIVNDHKTYKKRRSSHAHTNNFAKSVVNLVDSIYKEQLNTRVLAVALVETWTEKDID 360
Qy 361 ITTNPVQMLHEFSKYRORIKOHADAVHLISRYTFHYKRSLSYFGVCSRTGVCVNEYG 420
Db 361 ITTNPVQMLHEFSKYRORIKOHADAVHLISRYTFHYKRSLSYFGVCSRTGVCVNEYG 420
Qy 421 LPMVAOVAVLSQSLAONLGIOMEPSRRPKCDCTESWGGCIMEETGVSHSRKFSKCSILEY 480
Db 421 LPMVAOVAVLSQSLAONLGIOMEPSRRPKCDCTESWGGCIMEETGVSHSRKFSKCSILEY 480
Qy 481 RPLORGGACLFNRPRTKLFEPTECGNGVYEAEGECDCGFHVECYGLCKKCSLSNGAHC 540
Db 481 RPLORGGACLFNRPRTKLFEPTECGNGVYEAEGECDCGFHVECYGLCKKCSLSNGAHC 540
Qy 541 SDGPCNNNTSCLFOPRGYECRDVNECDITEYCTGDSGQCPNMLHODGYACNONOGRCY 600
Db 541 SDGPCNNNTSCLFOPRGYECRDVNECDITEYCTGDSGQCPNMLHODGYACNONOGRCY 600
Qy 601 NGECKTRDNOCQYIMGTAKGSDKFCYEKLTETEGENCGKGDWRMIQCSKHDFCGFL 660
Db 601 NGECKTRDNOCQYIMGTAKGSDKFCYEKLTETEGENCGKGDWRMIQCSKHDFCGFL 660
Qy 661 LCTNLTRAPRIGOLGELIPTSEYHOGRVIDCSGAHVLDLDDTVGYVEDEGTGCGPSMMC 720
Db 661 LCTNLTRAPRIGOLGELIPTSEYHOGRVIDCSGAHVLDLDDTVGYVEDEGTGCGPSMMC 720
Qy 721 LDRKCLIOALNMSSCPDLSKGYCSGHGVSNEATCICDTWAGTDCSIRDPVRNLHP 780
Db 721 LDRKCLIOALNMSSCPDLSKGYCSGHGVSNEATCICDTWAGTDCSIRDPVRNLHP 780
Qy 781 KDEGPKGSPATNLLIGSISAGAILVAAILVGGTGMGFKNVKRRRDPDPOQGP 832
Db 781 KDEGPKGSPATNLLIGSISAGAILVAAILVGGTGMGFKNVKRRRDPDPOQGP 832

RESULT 3
US-10-126-052A-325
: Sequence 325, Application US/10126052A
: GENERAL INFORMATION:
: APPLICANT: Murray, Richard
: APPLICANT: Aziz, Natasha
: TITLE OF INVENTION: Methods of Diagnosis of Lung Cancer, Compositions and
: FILE REFERENCE: 018501-001530US
: CURRENT FILING DATE: 2002-04-18
: PRIOR FILING DATE: 2001-04-18

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PRIOR APPLICATION NUMBER: US 60/290,492  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: US 60/339,245  
PRIOR FILING DATE: 2001-11-09  
PRIOR APPLICATION NUMBER: US 60/350,666  
PRIOR FILING DATE: 2001-11-13  
PRIOR APPLICATION NUMBER: US 60/334,370  
PRIOR FILING DATE: 2001-11-29  
PRIOR APPLICATION NUMBER: US 60/372,246  
PRIOR FILING DATE: 2002-04-12  
NUMBER OF SEQ ID NOS: 691  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 325  
LENGTH: 832  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-126-052A-325

Query Match 100.0%; Score 4553; DB 6; Length 832;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 832; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKPPGSSSRPPPLAGCSLAGASCPQGRGASVPASAPARTPPCRLVLLPLPLASS 60  
DB 1 MKPPGSSSRPPPLAGCSLAGASCPQGRGASVPASAPARTPPCRLVLLPLPLASS 60  
QY 61 RPRAMGAAPAPAPMNETAEKNLGLADEDNLTLOONSSSNTSYANMOKEITLPSRLTY 120  
DB 61 RPRAMGAAPAPAPMNETAEKNLGLADEDNLTLOONSSSNTSYANMOKEITLPSRLTY 120  
QY 121 INDDSESPYHVDTKARHQRKNRAVHLAQSFOLEAGSKFILDLLINGLSSDYVEI 180  
DB 121 INDDSESPYHVDTKARHQRKNRAVHLAQSFOLEAGSKFILDLLINGLSSDYVEI 180  
QY 181 HYEAGKPOYSKGGHCYHGSIRGVKDSKVALSTCNGHGMEDDTFYMIPELVLNDE 240  
DB 181 HYEAGKPOYSKGGHCYHGSIRGVKDSKVALSTCNGHGMEDDTFYMIPELVLNDE 240  
QY 241 KSTGRPHIIOKTLAAGYSKQKMLTMRGDMPELSELOMLKRRKRAVNSRGIEEMKY 300  
DB 241 KSTGRPHIIOKTLAAGYSKQKMLTMRGDMPELSELOMLKRRKRAVNSRGIEEMKY 300  
QY 301 LELMIVNDHKTYYKRRSSHAHTNNEFAKSVNLVDSIYEQLNTRVYLAVETWTERDOI 360  
DB 301 LELMIVNDHKTYYKRRSSHAHTNNEFAKSVNLVDSIYEQLNTRVYLAVETWTERDOI 360  
QY 361 ITTPVOMLHEFSKYRORIKQHADAVHLISRVTFYKRRSSLSYFEGVCSRTGAVNEYG 420  
DB 361 ITTPVOMLHEFSKYRORIKQHADAVHLISRVTFYKRRSSLSYFEGVCSRTGAVNEYG 420  
QY 421 LPMVAOVLQSOLAQNGLIOWEPSSRRPKDCCTESMGCCIMEETGVSHSRKSKSILEY 480  
DB 421 LPMVAOVLQSOLAQNGLIOWEPSSRRPKDCCTESMGCCIMEETGVSHSRKSKSILEY 480  
QY 481 RDLFQORGAGACLFNRPTKLEPTECGNGYVEAGEECDCGFHVECYGLCKKCSLSHAGC 540  
DB 481 RDLFQORGAGACLFNRPTKLEPTECGNGYVEAGEECDCGFHVECYGLCKKCSLSHAGC 540  
QY 541 SDGFCNNNTSCLFPRGREGRDVAVNECDITEYCTGDSQCCPNLHKOGYACNONMGX 600  
DB 541 SDGFCNNNTSCLFPRGREGRDVAVNECDITEYCTGDSQCCPNLHKOGYACNONMGX 600  
QY 601 NGECKTRDNOCQYIMGTAKAGSDKFCYEKLNTGTEKNGCKGDKGRWIOCSKHDVYCGTL 660  
DB 601 NGECKTRDNOCQYIMGTAKAGSDKFCYEKLNTGTEKNGCKGDKGRWIOCSKHDVYCGTL 660  
QY 661 LCTNLTRAPRIGOLGELIPTSFYHOGRVIDCSGAHVVLDDDTDVGYVEDGTPCPSMWC 720  
DB 661 LCTNLTRAPRIGOLGELIPTSFYHOGRVIDCSGAHVVLDDDTDVGYVEDGTPCPSMWC 720  
QY 721 LDRKCLQIOALNMSSCPILDSKGVCSGHGVSNEATICIDFTWAGTDCSIRPVRNLHP 780  
DB 721 LDRKCLQIOALNMSSCPILDSKGVCSGHGVSNEATICIDFTWAGTDCSIRPVRNLHP 780

QY 781 KDEGPKPSATNLIIISAGAILVAIVLGTGCGFKNVKKRRFPDTPQGP 832  
DB 781 KDEGPKPSATNLIIISAGAILVAIVLGTGCGFKNVKKRRFPDTPQGP 832

RESULT 4  
US-09-949-016-11203

Sequence 11203, Application US/09949016

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 11203

LENGTH: 686

TYPE: PRT

ORGANISM: Human

US-09-949-016-11203

Query Match 80.6%; Score 3669; DB 5; Length 686;  
Best Local Similarity 100.0%; Pred. No. 1,2e-277;  
Matches 662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 GLSSSYVELHENGKPOYSKGGHCYHGSITGVYDSKVALSTCNGHGMEDDTFYVM 230  
DB 25 GLSSSYVELHENGKPOYSKGGHCYHGSITGVYDSKVALSTCNGHGMEDDTFYVM 84  
QY 231 IEPLELVHBEKSTGRPHIIOKTLAAGYSKQKMLTMRGDMPELSELOMLKRRKRAVNP 290  
DB 85 IEPLELVHBEKSTGRPHIIOKTLAAGYSKQKMLTMRGDMPELSELOMLKRRKRAVNP 144  
QY 291 SNGIEEMKYLELMIVNDHKTYYKRRSSHAHTNNEFAKSVNLVDSIYEQLNTRVYLA 350  
DB 145 SNGIEEMKYLELMIVNDHKTYYKRRSSHAHTNNEFAKSVNLVDSIYEQLNTRVYLA 204  
QY 351 EMTWTERDOIITTPVOMLHEFSKYRORIKQHADAVHLISRVTFYKRRSSLSYFEGVCSR 410  
DB 205 EMTWTERDOIITTPVOMLHEFSKYRORIKQHADAVHLISRVTFYKRRSSLSYFEGVCSR 264  
QY 411 TFGVGVNEGLPMAVAOVLQSOLAQNGLIOWEPSSRRPKDCCTESMGCCIMEETGVSHSR 470  
DB 265 TFGVGVNEGLPMAVAOVLQSOLAQNGLIOWEPSSRRPKDCCTESMGCCIMEETGVSHSR 324  
QY 471 KFSKCSILEYRDLFQORGAGACLFNRPTKLEPTECGNGYVEAGEECDCGFHVECYGLCK 530  
DB 325 KFSKCSILEYRDLFQORGAGACLFNRPTKLEPTECGNGYVEAGEECDCGFHVECYGLCK 384  
QY 531 KCSLSHAGCSDGPPCCNNNTSCLFPRGREGRDVAVNECDITEYCTGDSQCCPNLHKODGY 590  
DB 385 KCSLSHAGCSDGPPCCNNNTSCLFPRGREGRDVAVNECDITEYCTGDSQCCPNLHKODGY 444  
QY 591 ACNONGRCYNGECKTRDNOCQYIMGTAKAGSDKFCYEKLNTGTEKNGCKGDKGRWIOCS 650  
DB 445 ACNONGRCYNGECKTRDNOCQYIMGTAKAGSDKFCYEKLNTGTEKNGCKGDKGRWIOCS 504  
QY 651 SKHDVYCGTLNTRAPRIGOLGELIPTSFYHOGRVIDCSGAHVVLDDDTDVGYVED 710  
DB 505 SKHDVYCGTLNTRAPRIGOLGELIPTSFYHOGRVIDCSGAHVVLDDDTDVGYVED 564  
QY 711 GTPCPSMWCIDRKCLQIOALNMSSCPILDSKGVCSGHGVSNEATICIDFTWAGTDCS 770  
DB 565 GTPCPSMWCIDRKCLQIOALNMSSCPILDSKGVCSGHGVSNEATICIDFTWAGTDCS 624



OY 771 RDEVRNHPKDEGPKSPATNLLIGSAGAILVAIVLGGTGWGKRNKKRRRDEFTQOG 830  
| | | | |  
Db 625 RDPVRNHPKDEGPKSPATNLLIGSAGAILVAIVLGGTGWGKRNKKRRRDEFTQOG 684  
OY 831 PI 832  
| |  
Db 685 PI 686

RESULT 5  
US-09-724-676-80847  
; Sequence 80847, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 80847  
; LENGTH: 870  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-724-676-80847

Query Match 43.6%; Score 1985.5; DB 5; Length 870;  
Best Local Similarity 47.5%; Pred. No. 4.3e-146;  
Matches 388; Conservative 121; Mismatches 227; Indels 81; Gaps 14;

OY 36 SAPARTPCRLIVLILPPLAASSPRAMGAAPSAFPMNETAKNLGVLADENITLQ 95  
| | | | |  
Db 3 AAVAVSPFLILCVLGTCPARC-----GQAGDASIMLEEKREN----- 42  
OY 96 NSSSNISYSNAKREITLPSRLIYYINODSESPYHVLDTKARHQQKHNKAVHIAQASFQI 155  
| | | | |  
Db 43 -----REVERQSIYPLRLIYRSGGDESRHIALDTRKGLGROLTHVDAQSFQY 93  
OY 156 EAFGSKFLDILNNGLLSSDYVEIHYEN-GKPOYSKGEHCYHGSIRGVKDSKVALST 214  
| | | | |  
Db 94 DAFGTSFLDVLNHDLLSSEYIERHIEHGKTYEVGGEHCYQGHIRGNPDSFVALST 153  
OY 215 CNGLHGFEDDTFYVIEPLELVHDEKSTGRP-----HIQKTLAQSYSK-----OMKN 263  
| | | | |  
Db 154 CHGLHGFEDDTFYVIEPLELVHDEKSTGRP-----HIQKTLAQSYSK-----OMKN 263  
OY 264 LTMERGQMPFLSELQWLKRRKRAVNPSRGIFEEMKYLEIMIVNDHKTYYKRRSHAHNTN 323  
| | | | |  
Db 209 ITPSK-----FILKPRKRSKROLRRYPRVVEETKYIELMIVNDHLMFKHRLSVYHTN 263  
OY 324 NFAKSVNLVDSIYKEQNLNRYVLVAVETWEKQDITTPVQMLHEESKYRQR-IKOH 382  
| | | | |  
Db 264 TYAKSVNMADLLIKKQOLKTRIVLAMEWTADNKAISENPLTLTLREFMKYRDFIKER 323  
OY 383 ADAVHLISRVTFHYKRRSLSYFGVCSRTRGVGNENYGLPMAVAQVLSQSLAONLQIOME 442  
| | | | |  
Db 324 SDAVHLFSSGQFESSRGAAYIGICSLKGGGVNFEKTDLMAVTLAOSLAHNIGI--- 380  
OY 443 PSSRKPK-----CDCTSWGGCIMEETGVSHSRKFSKCSILEYRDLQRGAGACLFENRPT 497  
| | | | |  
Db 381 -ISDKRLASGECKCEDTWSGCMIGDTGYLPRKFTQCNIEEYHDFLNSGGACCLFNPS 439  
OY 498 KLEFTEPCNGVYVGEEDCGCFHVECY---GLCKKCSLSGAICSOGPCCNNTSCLFQ 554  
| | | | |  
Db 440 KILDPEPCNGVYVGEEDCGCFHVECY---GLCKKCSLSGAICSOGPCCNNTSCLFQ 554  
OY 555 PRGIECDVAVNECDITETGDSGCPPLNLRKQDYACNONOGRVNECKTRDNQCYI 614  
| | | | |  
Db 498 PRGIECDVAVNECDITETGDSGCPPLNLRKQDYACNONOGRVNECKTRDNQCYI 614  
OY 615 WGTKAAGSDKFCYEKLTNTEGTEKNGKCGKDGKRWIOCSHDPFCGGLCTNLTRAPRIQOL 674  
| | | | |

Db 558 WQKVTASDKYCYEKLNTIEGTEKNGKDGKDKTWTQCNKRDVLCGYLICTNIGNIPRLGEL 617  
OY 675 QCEIIFPTFYHQGRIDSCGAHVVLDDPTDVGYVEDGTPCGSPSMCLDRKCLQIOLNMS 734  
| | | | |  
Db 618 DGEITSTLVQOQGRNLCSGSHVYKLEEDVDLGYVEDGTPCGSPSMCLDRKCLQIOLNMS 677  
OY 735 SCPLDSKRGVCSGHCNENATCICDFTWAGTDCSINDPVRNHPKDEBPK----- 786  
| | | | |  
Db 678 TGLSKBEGTICSGNVCNENLACYCNRAHWIGSDC-----NTYFPHNDAKTGITLSCN 730  
OY 787 GPSATNLLIGSAGAILVAIVLGGTGWGKRNKKRR 823  
| | | | |  
Db 731 GVAQTNIIIGIAGTILVAILLIGITFAMGYKNVREQR 767

RESULT 6  
US-09-724-676A-80847  
; Sequence 80847, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676A  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 80847  
; LENGTH: 870  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-724-676A-80847

Query Match 43.6%; Score 1985.5; DB 5; Length 870;  
Best Local Similarity 47.5%; Pred. No. 4.3e-146;  
Matches 388; Conservative 121; Mismatches 227; Indels 81; Gaps 14;

OY 36 SAPARTPCRLIVLILPPLAASSPRAMGAAPSAFPMNETAKNLGVLADENITLQ 95  
| | | | |  
Db 3 AAVAVSPFLILCVLGTCPARC-----GQAGDASIMLEEKREN----- 42  
OY 96 NSSSNISYSNAKREITLPSRLIYYINODSESPYHVLDTKARHQQKHNKAVHIAQASFQI 155  
| | | | |  
Db 43 -----REVERQSIYPLRLIYRSGGDESRHIALDTRKGLGROLTHVDAQSFQY 93  
OY 156 EAFGSKFLDILNNGLLSSDYVEIHYEN-GKPOYSKGEHCYHGSIRGVKDSKVALST 214  
| | | | |  
Db 94 DAFGTSFLDVLNHDLLSSEYIERHIEHGKTYEVGGEHCYQGHIRGNPDSFVALST 153  
OY 215 CNGLHGFEDDTFYVIEPLELVHDEKSTGRP-----HIQKTLAQSYSK-----OMKN 263  
| | | | |  
Db 154 CHGLHGFEDDTFYVIEPLELVHDEKSTGRP-----HIQKTLAQSYSK-----OMKN 263  
OY 264 LTMERGQMPFLSELQWLKRRKRAVNPSRGIFEEMKYLEIMIVNDHKTYYKRRSHAHNTN 323  
| | | | |  
Db 209 ITPSK-----FILKPRKRSKROLRRYPRVVEETKYIELMIVNDHLMFKHRLSVYHTN 263  
OY 324 NFAKSVNLVDSIYKEQNLNRYVLVAVETWEKQDITTPVQMLHEESKYRQR-IKOH 382  
| | | | |  
Db 264 TYAKSVNMADLLIKKQOLKTRIVLAMEWTADNKAISENPLTLTLREFMKYRDFIKER 323  
OY 383 ADAVHLISRVTFHYKRRSLSYFGVCSRTRGVGNENYGLPMAVAQVLSQSLAONLQIOME 442  
| | | | |  
Db 324 SDAVHLFSSGQFESSRGAAYIGICSLKGGGVNFEKTDLMAVTLAOSLAHNIGI--- 380  
OY 443 PSSRKPK-----CDCTSWGGCIMEETGVSHSRKFSKCSILEYRDLQRGAGACLFENRPT 497  
| | | | |  
Db 381 -ISDKRLASGECKCEDTWSGCMIGDTGYLPRKFTQCNIEEYHDFLNSGGACCLFNPS 439  
OY 498 KLEFTEPCNGVYVGEEDCGCFHVECY---GLCKKCSLSNANHSQSDPCCNNTSCLFQ 554  
| | | | |  
Db 440 KILDPEPCNGVYVGEEDCGCFHVECY---GLCKKCSLSNANHSQSDPCCNNTSCLFQ 554  
OY 555 PRGIECDVAVNECDITETGDSGCPPLNLRKQDYACNONOGRVNECKTRDNQCYI 614  
| | | | |

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Db 498 PMGTVCRAVNDCCDIRETCGNSSQCAPNHHKMDYSCDVGOCICFGRCRCKTRDROCKYI 557
Oy 615 WGTKAAGSKFCYEKLTGTEKNGCKGKDRWIOCSKHDFEGLLCTNLTRAIRIGOL 674
Db 558 WQOKVTASDKYCEKLTGTEKNGCKGKDRWIOCSKHDFEGLLCTNLTRAIRIGOL 617
Oy 675 OGEIPTSFYHOGRAVDCSGAHVLDLDDTVGVGVEGCTPCGSPMCLDRKCLQIOALNMS 734
Db 618 DGEITSTLVVQGGRTLNCSGGHVKKLEEDVDLGYVEDGTCGPOMKLEHRCPLVASFNFS 677
Oy 735 SCPLDSKGVCSGHGVCSENEATCICDFTWAGTDCSIRDPVRLHPKDEGPK----- 786
Db 678 TGLSKRGTCISGNGVCSNKLKVCNRMHIGSDC-----NTYFPINDAKTGITLSGN 730
Oy 787 GPSATNLIIGSIAGAILVAIVLGGTGKGFKNVKKRR 823
Db 731 GVAGTNIIGIIGTILVLAIVLIGITAMGYKNVREOR 767

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## RESULT 7

```

PCT-US03-04508-64
Sequence 64, Application PC/TUS0304508
GENERAL INFORMATION:
APPLICANT: IDEC PHARMACEUTICALS
APPLICANT: GATELY, DENNIS
TITLE OF INVENTION: PROSTATE SPECIFIC GENES AND THE USE THEREOF IN DESIGN
FILE REFERENCE: 037003/0301985
CURRENT APPLICATION NUMBER: PCT/US03/04508
CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: 60/357,140
PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 60/396,082
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 60/386,759
PRIOR FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 93
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 64
LENGTH: 899
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US03-04508-64

```

```

Query Match 43.6% Score 1983.5; DB 1: Length 899;
Best Local Similarity 47.5% Pred. No. 6,4e-146;
Matches 388; Conservative 121; Mismatches 227; Indels 81; Gaps 14;

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Oy 36 SAPARTPCRLILVLLPLLAASSRRPAAAPAPAHMNETAEKNLGVLADEEDNTLQO 35
Db 3 AAVAVSVPLLLCVCITCPCPARC-----GQAGDASLMELEKREN----- 12
Oy 96 NSSSNISYSNAMOKETLPSRLIYINODESPYHVLDTKARHQQHKAHLAQAQSFJ1 155
Db 43 -----RFEKRGISIVPLRLIYRSGGEDESHDLDTRRGDGLGPQLTHVDAQSFYV 93
Oy 156 EAFGSKFILDILNNGLSSDYVEIHYEN-GKPOYSKGEHCYHGSIRKVKSKVALST 214
Db 94 DAFGTSFILDVVLNHLSEYIERHIEHGKTVKVEYKGGHCYQGIKRNPSFVALST 153
Oy 215 CNGLHGMFDDTFVYVIEPLELHVHDEKSTGRP-----HIQKTLAGQYSK-----OMKN 263
Db 154 CNGLHGMFDDTFVYVIEPLELHVHDEKSTGRP-----HIQKTLAGQYSK-----OMKN 263
Oy 264 LTMERCDQPPFSELOMLKRRRAVNPSCIFEDMKYLELMIVNDKRTYKHSSNAHFN 323
Db 209 ITPSK-----FIKPPPKRSKRLRRYPRNVEETRYIELMIVNDHLMFKHSLSVYHCN 263
Oy 324 NFAKSVNLVDSYKXOLNTRVLAVENTEKQDIDITNPQOMLHEFSKYROR-1KOH 382
Db 264 TTAHSVNMADLIYKQDLKTRIVLAMEWTATDNKFAISENPPLITREFMKRYRDPFKIK 323

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Oy 383 ADAVHLISRYTFPHYKRRSLSPFGVCSRTRGVGVNEXGLPMAAVLAQVLSQSLAQIOWE 442
Db 324 SDAVHLEFSSQFESSRRGAVIGIGICSLKGGVNERGKIDMAVTLAQSILAHNIGT--- 380
Oy 443 PSSRRKP-----CDCTESWGCIMETGVSHSRKFSKSLLEYRDLQRCGACLEFRPT 497
Db 381 -ISDKRLAAGECKCEDTWSGCIJMGDGYVLPKFKTQCNIEEYHDFLNSGGACLPFKPS 439
Oy 498 KLEPPECGNGVYEAAGECCCGFRVBCY-----GLCCRKCSLSNAGHSDGRCNNITSLQ 554
Db 440 KLDLPPRCGNGFLETGECDCGTPRAECVLGAECCCKCTTLTQDSQSDGJCK--KKFQ 497
Oy 555 PRGVECDVAVNEDITFCYTGDSQCPRLNKHODGVACNONOGVCYGECKTRPNOCYI 614
Db 498 PMGTVCRAVNDCCDIRETCGNSSQCAPNHHKMDYSCDVGOCICFGRCRCKTRDROCKYI 557
Oy 615 WGTKAAGSKFCYEKLTGTEKNGCKGKDRWIOCSKHDFEGLLCTNLTRAIRIGOL 674
Db 558 WQOKVTASDKYCEKLTGTEKNGCKGKDRWIOCSKHDFEGLLCTNLTRAIRIGOL 617
Oy 675 OGEIPTSFYHOGRAVDCSGAHVLDLDDTVGVGVEGCTPCGSPMCLDRKCLQIOALNMS 734
Db 618 DGEITSTLVVQGGRTLNCSGGHVKKLEEDVDLGYVEDGTCGPOMKLEHRCPLVASFNFS 677
Oy 735 SCPLDSKGVCSGHGVCSENEATCICDFTWAGTDCSIRDPVRLHPKDEGPK----- 786
Db 678 TGLSKRGTCISGNGVCSNKLKVCNRMHIGSDC-----NTYFPINDAKTGITLSGN 730
Oy 787 GPSATNLIIGSIAGAILVAIVLGGTGKGFKNVKKRR 823
Db 731 GVAGTNIIGIIGTILVLAIVLIGITAMGYKNVREOR 767

```

## RESULT 8

```

US-60-453-135-13204
Sequence 13204, Application US/60453135
GENERAL INFORMATION:
APPLICANT: CARCILL, Michele
APPLICANT: TAKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001456
CURRENT APPLICATION NUMBER: US/60/453,135
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13204
LENGTH: 775
TYPE: PRT
ORGANISM: Homo sapiens
US-60-453-135-13204

```

```

Query Match 43.6% Score 1983; DB 7: Length 775;
Best Local Similarity 48.7% Pred. No. 5,9e-146;
Matches 398; Conservative 92; Mismatches 225; Indels 102; Gaps 17;

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```

Oy 46 LLLVLLPLLAASSRRPRA--WGA-----AAPAPAHMNETAEKNLGVLADEEDNTLQONSSS 99
Db 12 LLLSLPLTPGLTGGPGAGLRMGGLPOLGCFAP----- 45
Oy 100 NISYSNAMOKETLPSRLIYINODESPYHVLDTKARHQQHKAHLAQAQSFJ1 155
Db 46 -----EVEPSSRLVRE--SSGGEVARKQOOLTRVROEPRGGRPHLAQVSVIAFN 94
Oy 160 SKPLDILNLNGLSSDYVEIHY-ENKGPQYSK-GEHCYHGSIRKVKSKVALSTCNG 217
Db 95 SNFPLDELNLNHLSSQYVERHFSRGTQSHSTAGCHCYQGIKRNPSFVALSTCOG 154
Oy 218 LHMFEEDDTFVYVIEPLELHVHDEKSTGRPHIIOKTLAAGYSKOMNLTMERCDQPPF 275
Db 155 LHGVFSGNLTYIVPEQVAGPWCAPGOLPHLTYR-----PL 194
Oy 276 SELQWLK-----RRKRAVNPSCIFEDMKYLELMIVNDKHTY 312

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Db      195 PDLGREGPCLFVAVPQASAPNRPRLRRKQVR--RGHPTVHSETKYVELIVINDHOLF 252
OY      313 KKRSHAHNTNNFAKSVNVLVDSTYKEQLNTRVLAVENTEMEDODITNPOMLHEEF 372
Db      253 EQMRQSVLLTSNFAKSVNLADVIYKEQLNTRVLAVENTEMEDODITNPOMLHEEF 312
OY      373 SKYROR--IKOHADAVHLISRVTFHKKRSSLSYFGVCSRTGAVGNEYGLPMAVAQVLSQ 431
Db      313 MYRREGLPSPDATHLFGSRTFOSTSSGAAYVGGICSLSHGCGVNEYGNMGAMAVTLAQ 372
OY      432 SLAONLGIOW--EPSSRRKPCDCTESWGCGIMEETGVSHSRKFSKSLLEYRDFLORGGGA 490
Db      373 TLGONLGMNMNKHRSAGDCKCPDIMGCLMEDTGFYLPKRFKSCSIDETYNOLFDEGGGS 432
OY      491 CLFNRPRTKLEPTEGNGVYEAEGECDCGFHVECY---GLCKKCSLSNGAHCSGDPCCN 547
Db      433 CLFNKPKLDDPPEGNGFVEAGEECDCGVSQECSSRAGNCKKCTLTHDAMCSGDLCCR 492
OY      548 NTSCLEPFGYECDAVNECDITTEYCTGDSGCPNHLKODGYACNONOGRCYNECKTR 607
Db      493 R--CKYERGVSCREAVNECDIAETCTGDSGCPNHLKIDGYCDHOGRCYGGRCRTR 550
OY      608 DNOCOYIMGTAKASDCKFCYEKLNTEGTEKNGCGDGMWIOCSKHDFVCGFLCTNLR 667
Db      551 DRCCOVLNMGHAAA--DRFCYEKLNTEGTERGSCGKRGSGWVQCSKODVLCGFLCTNLSG 608
OY      668 APRIGOLGEIIPTSFYHOGRAVIDSAGAHVLDLDDTGVYEDGTPCGPSMMLCDLRKCLQ 727
Db      609 APRIGDLVDISSVTFYHOGKELDRCGHVOLDGSDLSYVEDGTACGPNMLCDLRCLP 668
OY      728 IQALNMSSCPDLSKCKVCSGHGVCSEATCICDFTWAGDCTSRDPVRNLHP--KDEGRK 786
Db      669 ASAFNFSTCPGSGERRICSHHGVCSENEKCICDPMTGKDCSTHNPPTSPTGETERYK 728
OY      787 GPSATNLIIGSIAGAILVAIVLGGTGWGFKNVKRR 823
Db      729 GPSGTNIIIGSIAGAVLVAIVLGGTGWGFKNIRRR 765

RESULT 9
US-60-453-050-13204
; Sequence 13204, Application US/60453050
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: LUKE, May
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001457
; CURRENT APPLICATION NUMBER: US/60/453,050
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 13204
; LENGTH: 775
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-60-453-050-13204

Query Match      43.6%; Score 1983; DB 7; Length 775;
Best Local Similarity 48.7%; Pred. No. 5.9e-146;
Matches 398; Conservative 92; Mismatches 225; Indels 102; Gaps 17;

OY      46 LLLVLLPLPLAASSRRA--MGA---AAPAPPHNMTAEKNLGLVLADEDNTLQONSSS 99
Db      12 LLLSLPLTPBLGOGPRGALRMGLPQLGGPAP----- 45
OY      100 NISYSNMAKKEITPLSLIYINODSEPYHVLDTKARHQAQKNAVHLAQASFOIAFG 159
Db      46 -----EVEPSRLVRE--SSGGEVRKCOOLDTRVROEPPGPPVHLAQVSVFVAFN 94
OY      160 SKPTLIDLNLNGLSSDYVEIHY--ENGKPOYSKG--GEHCYHGSIRGVKDSKVALSTGNG 217

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Db      95 SNFTLDELNLNHLHLSQYVERHFRSECTOHSAGDCHCYOGKLRGNPHSFAALSTGCG 154
OY      218 LHGMFEDDTFYMYTEPLELV--HDEKSTGRPHILQKLAGOYSQOMKNTMERGDOWPFL 275
Db      155 LHGVSDGNLTYIVEPDEVAGPMGAPQGLPHLYRT-----PLL 194
OY      276 SELQMK-----RRKRVNPSRG--IFEMKYLELIMVNDHKTY 312
Db      195 PDLGREGPCLFVAVPQASAPNRPRLRRKQVR--RGHPTVHSETKYVELIVINDHOLF 252
OY      313 KKRSHAHNTNNFAKSVNVLVDSTYKEQLNTRVLAVENTEMEDODITNPOMLHEEF 372
Db      253 EQMRQSVLLTSNFAKSVNLADVIYKEQLNTRVLAVENTEMEDODITNPOMLHEEF 312
OY      373 SKYROR--IKOHADAVHLISRVTFHKKRSSLSYFGVCSRTGAVGNEYGLPMAVAQVLSQ 431
Db      313 MYRREGLPSPDATHLFGSRTFOSTSSGAAYVGGICSLSHGCGVNEYGNMGAMAVTLAQ 372
OY      432 SLAONLGIOW--EPSSRRKPCDCTESWGCGIMEETGVSHSRKFSKSLLEYRDFLORGGGA 490
Db      373 TLGONLGMNMNKHRSAGDCKCPDIMGCLMEDTGFYLPKRFKSCSIDETYNOLFDEGGGS 432
OY      491 CLFNRPRTKLEPTEGNGVYEAEGECDCGFHVECY---GLCKKCSLSNGAHCSGDPCCN 547
Db      433 CLFNKPKLDDPPEGNGFVEAGEECDCGVSQECSSRAGNCKKCTLTHDAMCSGDLCCR 492
OY      548 NTSCLEPFGYECDAVNECDITTEYCTGDSGCPNHLKODGYACNONOGRCYNECKTR 607
Db      493 R--CKYERGVSCREAVNECDIAETCTGDSGCPNHLKIDGYCDHOGRCYGGRCRTR 550
OY      608 DNOCOYIMGTAKASDCKFCYEKLNTEGTEKNGCGDGMWIOCSKHDFVCGFLCTNLR 667
Db      551 DRCCOVLNMGHAAA--DRFCYEKLNTEGTERGSCGKRGSGWVQCSKODVLCGFLCTNLSG 608
OY      668 APRIGOLGEIIPTSFYHOGRAVIDSAGAHVLDLDDTGVYEDGTPCGPSMMLCDLRKCLQ 727
Db      609 APRIGDLVDISSVTFYHOGKELDRCGHVOLDGSDLSYVEDGTACGPNMLCDLRCLP 668
OY      728 IQALNMSSCPDLSKCKVCSGHGVCSEATCICDFTWAGDCTSRDPVRNLHP--KDEGRK 786
Db      669 ASAFNFSTCPGSGERRICSHHGVCSENEKCICDPMTGKDCSTHNPPTSPTGETERYK 728
OY      787 GPSATNLIIGSIAGAILVAIVLGGTGWGFKNVKRR 823
Db      729 GPSGTNIIIGSIAGAVLVAIVLGGTGWGFKNIRRR 765

RESULT 10
US-09-949-016-7314
; Sequence 7314, Application US/09949016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 7314
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-7314

Query Match      43.4%; Score 1976.5; DB 5; Length 772;
Best Local Similarity 47.5%; Pred. No. 1.9e-145;

```

	Matches	386,	Conservative	118:	Mismatches	229:	Indels	81:	Gaps	14:
Oy		31	GSVPASAPARTPPCCALLVLLLPPLAASSRRPAMCAAPSAPHNNETLEKNLGVLADEE	90						
Dd		9	GSTMAAAVAVSPELLLCVLCTGCPARC-----GAQDASIMELERKEN-----	53						
Oy		91	NTLQONSSNISYSNAOKEITLPRLIYYINODESPRHVIDTKRHOQKHNKAVALAO	150						
Dd		54	-----RVEROSIVPLRLIYRSGCEDSRDALDTRRGDLGGCQLTHVDQ	99						
Oy		151	ASFQIEAFGSKFILDILANGLSSDYVEIHEN-GKPOYSKGEGCYUHGSIQVWDSK	209						
Dd		100	ASFQVDAAGTSFTILDVNLNHDLSSEYIERHTEHGKTVEAKGGEHCYOGHIRGNDFSR	159						
Oy		210	VALSTCNLHGFEEDTFYMIETPELVNDEKSTGR-----HIQKTLAQOYSK-----	259						
Dd		160	VALSCHGHGHEFYQGNHTYLTP-----EENDTQODEHFHSVKSRULEFSLDLPSE	214						
Oy		260	-QMKNLTIERGDQWPFLSELQWLKRKKRAVNRSRGIFEEMKYLELMIVNDHKYKRRSS	318						
Dd		215	FQOVNITPSK-----FILKPRKRSKQROLRARPRNVEETKYIELMIVNDHLMKKHRLS	269						
Oy		319	HAHTNPFKSVYNLVDSITYKEOLNTRVULVAVETWEKOJIDTTNPVOMLFESFYRQR	378						
Dd		270	VVHTNTYAKSVYNMADLYIKDQLKRIYLVAMETATMDKFAISENPILTTLREFMYRRD	329						
Oy		379	-IKOHADVHLISRTYFNHKRSSLSYFGVCSTRGYVNEGLPMAAVOVLISOALOND	437						
Dd		330	FIKESDVAHLFESSGFESSRSGAAYIGICSLUKGGVNEGKTDMLAVTLAQSIAHNI	389						
Oy		438	GIOWEPSSRPK-----CDCTESWGCIIMEETGVSHSRFSKCSILEYRDPIORGGAQL	492						
Dd		390	GI-----IDKRLKLASGECKCEDTWGACIMGDTGYULPKFKTCOCINEEYHDFLNSGGACL	445						
Oy		493	FNRPKLESEPPECGGYVAGEECOCGFIVECY---GLCCCKCSLSNGAHSCSPGCCNNT	549						
Dd		446	FNKPBLDIPRECNGFLETGECOCGPBAECVLEGABECKCTLTLODOSQSDGLOCK--	503						
Oy		550	SCLFOPRCYEGRDAVNECDITEYCTGDSQGCPNLHKODGYACNONOGRNYNECKTRDN	609						
Dd		504	KCFOPMGTVCEAVNDCDIRETCSGNSOCAPIHHKMGGYSCDGOYGICFGRCRKT RDR	563						
Oy		610	OCQYIWGRKAGSDKFYCEKLTBECTENGKNCGRKDDRMVQCASHDVPCGFLICTNLTLZAP	669						
Dd		564	OCKYIWGWKVYASDDYCYEKELINEETEKNGCKDKDQWTVMQNKRDVLGLGTLCTNGXJP	623						
Oy		670	RIGOLOGELIPTSFYHOGCRVIDCSAHVVLDDBDIVGYVEDGPPCGSPMMXCIDRKCIQJ	729						
Dd		624	RUGELDGETSTILVVOQGRTLNCSGHNVLLEEDVDLGTYVEDGPPCROPMMGLEHRELTJVA	683						
Oy		730	ALNMSSCPUDSKGKVCSGHGVCSENATYCICDFTWAGTDCSIRDVRYNLHPKDEGR---	786						
Dd		684	SNFSTCLSSKSGGTICSGNGVCNSNELKCVCNHMTGISDC-----NTFFPHNDAKTGII	736						
Oy		787	-----GPSATNLIISINGAILVAIYVGCGTMGRF	817						
Dd		737	TLSGNGVACTNITIIIGITILLVALLILGITANGXR	772						
RESULT 11										
US-09-949-016-7315										
Sequence 7315, Application US/09949016										
GENERAL INFORMATION:										
APPLICANT: VENTER, J. Craig et al.										
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED										
FILE REFERENCE: CL001307										
CURRENT APPLICATION NUMBER: US/09/949, 016										
PRIOR FILING DATE: 2000-04-14										
PRIOR APPLICATION NUMBER: 60/241,755										
PRIOR FILING DATE: 2000-10-20										
PRIOR APPLICATION NUMBER: 60/237,768										
PRIOR FILING DATE: 2000-10-03										

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: PRIOR APPLICATION NUMBER: 60/723,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SPO ID NOS: 207012
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SPO ID NO: 7315
: LENGTH: 772
: TYPE: PRT
: ORGANISM: Human
: US-09-949-016-7315

```

Query Match	43.48;	Score 1976.5;	DB 5;	Length 772;
Best Local Similarity	47.58;	Pred. No. 1.9e-145;		
Matches 388;	Conservative 118;	Mismatches 229;	Indels , 81;	Gaps 14;

```

0Y 31 GSVASAPARPPCLLVLLLPRLAASSRRRAGAAAPAPNNETAEKNVLGVLAED 90
Db 9 GSTMOAAVAVASVPFLLLCVLGCPCPARC-----GQAGDASIMELEKREK EN----- 53
0Y 91 NTLQOONSSNYSYNAAMKEITLPRLITYYINODESESYHYLDYTKARHQOKINKAVHLAQ 150
Db 54 -----REVEROSITVPLRLITYRSGDEDSRRDADLTVDYKODLGPOLTHDQ 99
0Y 151 ASFOIEAFSGKFIIDLINLNGLLSSDYVEIHEN-GKPOYSKGEGHYVHGSIRGVKDSK 209
Db 100 ASFOVDAGTSTIIDLVLNHDLLSEYIERNIEHOGKIVYEVKGGHCYQOIGHIRPNPSP 159
0Y 210 VALSTCNGLHGFEDDFVYMIETPELVHDEKSTGRP---HIQKTLAGQYSK----- 259
Db 160 VALSTCHGLHGFYDGHNTYLIETP-----EENDITQDEPFHFSYKSRLEFFESLDDPSE 214
0Y 260 -OMKNTLMERGOFMFLELDOMLKRRKRAVANSRQIEFEMKYLETIMTYNDHTYKXKHS 318
Db 215 FOQVNTYPSK-----FILKPRKRSKROLARYPRVVEETKYTEIMTYNDHLMFKHRIS 269
0Y 319 HAHTNNAFSAVYNLVDSTYKEDOLNRYVVLVAVETTERDQIDITPNPOMLIEFSKYROR 378
Db 270 VVHTTNTKASVYNNMADLTKYKQIKRITYLVAMETATONKFAISENPLITLAEFPAKYRRD 329
0Y 379 -IKOHADAVHLISRVTFFHKSSLSYFGCVGSKRTGCVNEYGLDPMAVOVLSSOLAOLN 437
Db 330 FIKESDSVAVHLFSGQFESSRSAGVAYIGGICSLGAGGVEBKTKDMLAVALTLAOSLAHNI 389
0Y 438 GIOWEPSSARKPK-----CDCTESMGCIMEETGYSHSRFSKCSITLEYRDFLORGGAGL 492
Db 390 GI-----ISDKRKLASGECKCEDTWSGCIIMGDTGYLLPKFTQCNIEETHNDFLNSGGACL 445
0Y 493 FNRPTKLEPTEPCGNGYVAGEEEDCGCFHVECY---GLQCKKCSLSNAGHSCSDGPCNNT 549
Db 446 FNKPSKLDLPPRCGNGFIETGEECDGGRABEVLBGABECKCKCTLPLDOSQSDGLCKK-- 503
0Y 550 SCLPSPRGYECRDVANECDITYETCTGDSGQCPRLNHKODGYACNONGRACYGSEKTRDN 609
Db 504 KCFEPQMTYVCEAVANDCDIRECTCGNSQOCAPNIIHKMDGYSCDVOVGICFCFGKCTRDR 563
0Y 610 QCOYIMTKRAAGSDKFCYEKLTETESTENGKNCARDKDDPMIOGSKHNVFGCGLICTJMYTRAP 669
Db 564 OCKTYIMGOKVYASDKTYCEKLTIEBTEGKNGCKODPMYIOCKKRYDLGCLYLLCTYINGRP 623
0Y 670 RIGQLOGEIIPTSFYHOGRVIDCSGAHVHLDLDDTVDYGVVEDGTPCGSPSMCLDRKCLQIQ 729
Db 624 RIGLEDGETITSLVYQOGRITLNCSGHAKLEEDVDVLGYVEDGTPCGPOIMCLENKCLRPVA 683
0Y 730 ALNMSSCPLDSDGKVCSGHVCVSNATYICDPTAGTACSTIROPVRNLHPRPDEGRP--- 786
Db 684 SFNESTCLSSKRGITCSGNGVCNKLKVCVNCNHHMGSDC-----NTYFPHNDAKKTGI 736
0Y 787 -----GSPATNLIISIGAILVAIVLGGTGMGRK 817
Db 737 TLSGNGVACTNIIITIGIAGTILVALIILGITAMGRK 772

```

Sequence 7316, Application us/09949016  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: fastseq for windows version 4.0  
SEQ ID NO 7316  
LENGTH: 772  
TYPE: PRF  
ORGANISM: Human  
US-09-949-016-7316

Query Match 43.4%; Score 1976.5; DB 5; Length 772;  
Best Local Similarity 47.5%; Pred. No. 1.9e-145;  
Matches 388; Conservative 118; Mismatches 229; Indels 81; Gaps 14;

OY 31 GVPASAPARTPCRLVLLPLLAASSRRAMGAAPSAPHMNETAEKNLGVLADED 90  
DB 9 GSTMAAIVAVSVFELLCVGTCPARC-----GAGDASLMELEKREN----- 53  
OY 91 NTLQONSSNISYNAKQKITLPSRLIYYINODSESPYHVDTKARHQQKHNKAVHLAQ 150  
DB 54 -----REVEROSIVPLRLIYRSNGEDESBDALDTRVGRDLGQPLTHVQ 99  
OY 151 ASFOEAFSGSKFLDLILNGLISDYVEIHYEN-GKPOYSKSGEHYHGSTRGVYDSK 209  
DB 100 ASFOVAFGTSFLDVLNHLDSIEYIERHIEHGKTYEVKGEHCYOGHIRGNPSF 159  
OY 210 VALSTNGLHGMEDDTFVYMEPLELVHDEKSTGRP---HIIOKTLAQSCK----- 259  
DB 160 VALSTGHLGHMFYDGNHYLIER-----ENDTTOEDFHFHSYKSLREFSLDLPSE 214  
OY 260 -QKNLTMERGDMPLSELQWLKRRRAVNPSSRGIFEENKYLEMLIVNDHKTYKRRSS 318  
DB 215 FQOVNITPSK-----FLKPRPKRSKQRLRRYPRNVEEFKYTELMIVNDHLMFKRHLS 269  
OY 319 HAITNFAKSVNLVDSIYKQULNTRVYLAVEWTEKDQIDITTNPVOMLHESKYROR 378  
DB 270 VVHTNTYAKSVNMADLTRYDQKTRIVLAVMETWATDNKFAISENPLITLREFMKYRD 329  
OY 379 -IKOHADAVHLISRVTFHYKRSLSYFGVCSRTRGVNEGYLPMVAQVLSQSLAQL 437  
DB 330 FIKKSDAVHLFGSGOFESSRSGAAYIGICSLKGGVNEFGKTDMAVTLAQSLSANI 389  
OY 438 GIOMESSSKRPK-----CDCTESWGCIMETGYSHRSKFSKCSILEYRDFLORGAGCL 492  
DB 390 GI-----ISDRKRLASGCEKCEDWSGCIMDGYLLPKFTQCNIIEYHDFLNSGGACL 445  
OY 493 FNRPTKLFEPTEGNGVVEAGEEDCGFHECY---GLCCKKSLSNGAHCSDPCCNNT 549  
DB 446 FNRPSKLLDPECGNGFIETGEBDCGTPAECVLEGAECCKKTLTODSQCSDGLCK-- 503  
OY 550 SCLFOPRGYECRAVNECDITTEYCTSDSGCPNLHRODGYACNQNOGRVCYNGECKTRDN 609  
DB 504 KCKFQPMGTVCRAEVNCDIRETCSGNSQCAPNIHMKMDYSGDGVGICFGGRCKTRDR 563  
OY 610 QCOQIMGTAKAGSDKFCYEKINTGTEKNGKGDGDMIOCSKHDFVCGFLCTNLTRAP 669  
DB 564 QCKYIMOKYATASDKYCEKINIEGTEKNGKGDWIOCNKRDVLCGYLLCTNIGNIP 623  
OY 670 RIGLOGEIILPTSYHGGRAVLDGSGAHVLDLDDTVDVGVEDGTPCGSPSMCLDRKCLIQ 729  
DB 624 RLGLDELITSTLVVQGRITLNSGSHVLEEDVLDGIVEGDTTCGGPOMCLBHRCLPYA 683

OY 730 ALNMSSCPILDSKGVCSGHCNSENATCICDFTWAGTDCSIRDPVNNLHPPKDEGPK--- 786  
DB 684 SFNFSTCLSKRECTICSGNVCNSELKVCNRRHWISSDC-----NTFPHNDAKTGT 736  
OY 787 -----GPSATNLIIGSIAGAILVAIVLGGTGWGFK 817  
DB 737 TLGNGVACTNIIIGIAGTILVALILGITAWGK 772

Search completed: June 1, 2003, 18:52:27  
Job time: 198 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2003, 16:58:30 : Search time 58 Seconds

(without alignments)  
422.067 Million cell updates/sec

Title: US-09-634-252a-4

Perfect score: 4553

Sequence: 1 MKPSSSRKQPLACGSLAG.....GWFKNVKKRRDPDQGP1 812

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

- 1: /cgcn2\_6/ptodata/1/1aa/5a\_COMB.pep.\*
- 2: /cgcn2\_6/ptodata/1/1aa/5b\_COMB.pep.\*
- 3: /cgcn2\_6/ptodata/1/1aa/5a\_COMB.pep.\*
- 4: /cgcn2\_6/ptodata/1/1aa/5b\_COMB.pep.\*
- 5: /cgcn2\_6/ptodata/1/1aa/5a\_COMB.pep.\*
- 6: /cgcn2\_6/ptodata/1/1aa/5b\_COMB.pep.\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3621	79.5	696	4	US-09-351-414-2
2	1978	43.4	769	1	US-08-243-542-4
3	1978	43.4	769	1	US-08-477-407-4
4	1978	43.4	769	1	US-08-484-355-4
5	1867.5	41.0	670	1	US-08-243-542-3
6	1867.5	41.0	670	1	US-08-477-407-3
7	1867.5	41.0	670	1	US-08-484-355-3
8	1297	28.5	524	1	US-08-243-542-2
9	1297	28.5	524	1	US-08-477-407-2
10	1297	28.5	524	1	US-08-484-355-2
11	1293	28.4	488	1	US-08-243-542-1
12	1293	28.4	488	1	US-08-477-407-1
13	1293	28.4	488	1	US-08-484-355-1
14	897	19.7	812	4	US-09-632-098-4
15	871	19.1	802	4	US-09-632-098-2
16	837	18.4	855	4	US-09-813-819-2
17	837	18.4	855	4	US-09-920-048-2
18	829	18.2	751	2	US-08-836-443-3
19	826	18.1	814	4	US-09-813-819-4
20	826	18.1	814	4	US-09-920-048-4
21	772.5	17.0	613	4	US-09-026-001A-10
22	766.5	16.8	621	4	US-09-026-001A-18
23	751.5	16.5	621	4	US-09-026-001A-6
24	749	16.5	592	4	US-09-026-001A-14
25	739	16.2	734	5	US-08-765-243-8
26	739	16.2	734	5	PCT-US95-07295-8
27	736	16.2	616	4	US-09-608-790-1

28	711	15.6	651	1	US-08-264-101-2	Sequence 2, Appl1
29	711	15.6	651	2	US-08-765-243-2	Sequence 2, Appl1
30	711	15.6	651	5	PCT-US95-07295-2	Sequence 2, Appl1
31	691	15.2	735	2	US-08-765-243-6	Sequence 6, Appl1
32	691	15.2	735	5	PCT-US95-07295-6	Sequence 6, Appl1
33	649	14.3	521	4	US-09-026-001A-12	Sequence 12, Appl1
34	611	13.4	462	4	US-09-026-001A-16	Sequence 16, Appl1
35	577.5	12.7	529	2	US-08-836-442-3	Sequence 3, Appl1
36	517	11.4	457	1	US-08-264-101-4	Sequence 4, Appl1
37	517	11.4	457	2	US-08-765-243-4	Sequence 4, Appl1
38	517	11.4	457	5	PCT-US95-07295-4	Sequence 4, Appl1
39	486.5	10.7	439	1	US-09-026-001A-8	Sequence 8, Appl1
40	392	8.6	470	1	US-08-514-014-2	Sequence 2, Appl1
41	392	8.6	470	2	US-08-833-823-2	Sequence 2, Appl1
42	392	8.6	470	3	US-08-813-150-2	Sequence 2, Appl1
43	389.5	8.6	464	4	US-09-411-329C-14	Sequence 14, Appl1
44	387.5	8.5	462	4	US-09-411-329C-3	Sequence 3, Appl1
45	387.5	8.5	462	4	US-09-411-329C-17	Sequence 17, Appl1

ALIGNMENTS

RESULT 1	US-09-351-414-2	Application US/09351414
Sequence 2, Appl1	Patent NO. 6265199	
GENERAL INFORMATION:		
APPLICANT:	Sheppard, Paul O.	
APPLICANT:	Baird, Nand	
APPLICANT:	Deisher, Theresa A.	
APPLICANT:	Bishop, Paul D.	
TITLE OF INVENTION:	DISINTEGRIN HOMOLOG	
FILE REFERENCE:	98-29	
CURRENT APPLICATION NUMBER:	US/09/351,414	
CURRENT FILING DATE:	1999-07-09	
NUMBER OF SEQ ID NOS:	13	
SOFTWARE:	FASTSEQ for Windows Version 3.0	
SEQ ID NO:	2	
LENGTH:	696	
TYPE:	PRO	
ORGANISM:	Homo sapiens	
US-09-351-414-2		
Query Match	79.5%	Score 3621; DB 4; Length 696;
Best Local Similarity	99.7%	Pred. No. 6.4e-291;
Matches	654;	Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	132	LDTKARHQKHNKAVHLAQAQSFQIEAFGSKFLDILNNGLLSSDYVEIHYENCKPQYSK 191
DB	9	LDTKARHQKHNKAVHLAQAQSFQIEAFGSKFLDILNNGLLSSDYVEIHYENCKPQYSK 68
QY	192	GGEHCYHGSIRGVKDSKVALSTCNGLGMEFEDDTFVYMIPELIVHDEKSTGRPHITOK 251
DB	69	GGEHCYHGSIRGVKDSKVALSTCNGLGMEFEDDTFVYMIPELIVHDEKSTGRPHITOK 128
QY	252	TIAQOYSKOMNLMERGDQWPLSELOMLRRKRAVPSCGIFEMMYLEIMVNDHKT 311
DB	129	TIAQOYSKOMNLMERGDQWPLSELOMLRRKRAVPSCGIFEMMYLEIMVNDHKT 188
QY	312	YKRRSSHAHTNFAKSVNLVDSTYKQQLTRVVLVAEVTWETKQDITTPVOMLHE 371
DB	189	YKRRSSHAHTNFAKSVNLVDSTYKQQLTRVVLVAEVTWETKQDITTPVOMLHE 248
QY	372	FSKYRQRIKQADAVHLISRTFHYKRSLSYFEGVCSRTGCVGNEGLPMAVAQVLSQ 431
DB	249	FSKYRQRIKQADAVHLISRTFHYKRSLSYFEGVCSRTGCVGNEGLPMAVAQVLSQ 308
QY	432	SIAONLGIOWPSSRRKPKCDCTESMGCCIMETGSHSRKSKSCSILEYRPFLOHGGGAC 491
DB	309	SIAONLGIOWPSSRRKPKCDCTESMGCCIMETGSHSRKSKSCSILEYRPFLOHGGGAC 368
QY	492	LFRPPTKLEPTEGCGNGYVEAGEBCDGFHWECYGLCKCKCSLSNGAHCSDBGCCNNTSC 551

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DB      369  LFNRPKLEFPEECGGVYEAEECCGCHVECYGLCKCKCSLSNAGHSDGQCNNITSC 428
OY      552  LFQPRGYECRDVANECDITEYCTGDSGQCPNHLKODGYACNONGRCVNGECKTRDNOC 611
DB      429  LFQPRGYECRDVANECDITEYCTGDSGQCPNHLKODGYACNONGRCVNGECKTRDNOC 488
OY      612  OYIWGTRKAAGSDKFCYEKLNTEGTEKNGCKGKDDRMWIOCKSHDVFPGFLLCTNLTAPRI 671
DB      489  OYIWGTRKAAGSDKFCYEKLNTEGTEKNGCKGKDDRMWIOCKSHDVFPGFLLCTNLTAPRI 548
OY      672  GLOGGLIPTSFYHOGRAVIDCSGAHVLLDDPDVGVVEGTGPGSPMMLCDRCLQIOL 731
DB      549  GLOGGLIPTSFYHOGRAVIDCSGAHVLLDDPDVGVVEGTGPGSPMMLCDRCLQIOL 608
OY      732  NMSGCLPSDKGKVCSGHGVCSNEATCICDFTTAGTDCSIRDPVRLNHPKDEGPKG 787
DB      609  NMSGCLPSDKGKVCSGHGVCSNEATCICDFTTAGTDCSIRDPVRLNHPKDEGPKG 664

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RESULT 2
US-08-243-542-4
: Sequence 4, Application US/08243542
: Patent No. 5552526
: GENERAL INFORMATION:
: APPLICANT: NAKAMURA, YUSUKE
: APPLICANT: EMI, MITSURU
: TITLE OF INVENTION: MDC PROTEINS AND DNAs
: TITLE OF INVENTION: ENCODING THE SAME
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
: STREET: 2026 Rambling Road
: CITY: Kalamazoo
: STATE: Michigan
: COUNTRY: USA
: ZIP: 49008-1699
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
: COMPUTER: IBM PC/XT/AT Compatible
: OPERATING SYSTEM: MS-DOS 5.0
: SOFTWARE: WordPerfect 5.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/243,542
: FILING DATE:
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 5-136602
: FILING DATE: 14 MAY 1993
: APPLICATION NUMBER: JP 5-257455
: FILING DATE: 22 SEPTEMBER 1993
: APPLICATION NUMBER: JP 6-49904
: FILING DATE: 23 FEBRUARY 1994
: APPLICATION NUMBER: JP 6-73328
: FILING DATE: 12 APRIL 1994
: APPLICATION NUMBER: JP 6-84470
: FILING DATE: 22 APRIL 1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Terryence F. Chapman
: REGISTRATION NUMBER: 32 549
: REFERENCE/DOCKET NUMBER: Furuya Case 1313
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (616) 381-1156
: TELEFAX: (616) 381-5465
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 769 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: IMMEDIATE SOURCE:

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: LIBRARY: human fetal brain cDNA library
US-08-243-542-4

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Query Match      43.4%; Score 1978; ~DB 1; Length 769;
Best Local Similarity 48.6%; Pred. No. 5,3e-155;
Matches 397; Conservative 93; Mismatches 225; Indels 102; Gaps 17;

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OY      46  LLLVLLLPPLAASRPRA--WGA----APASPHNNETAEKNLGLVLAEDDNTLQGNSSS 99
DB      12  LLLSLPTPGLGTQGPAGALRMWGLDQLGGGPAP----- 45
OY      100  NISYSNAMOKEITLPSRLIYINODESPYHVLTFRARHQOKHNKAVHLAQAFOLEAFG 159
DB      46  -----EYEPKSLVRE--SSGGEYVRQQLDTRRQEPGPPVHLAQAQVFAFN 94
OY      160  SKFILDILLNGLLSDSYEIRH--ENCKPOYSKG--GECHYHSGINGVDSKALSTCNG 217
DB      95  SNFTLDELHNLHLLSSQYVERHFSREGTQHSAGAGCHYQCKLRGNPHSFAALSTCOG 154
OY      218  LHGMFEDDTFYVMIPEELV--HDEKSTGRPHIIOKTLAQYQSKMKNLTMERGDMWPL 275
DB      155  LHGVFSDGNLTLYVEDEVAGPWGAPDGPLILYRT-----PLL 194
OY      276  SELQNLK-----RRRAVNSRG---IFEMKYLELMIIVNDRKTY 312
DB      195  PDLGCRPEBCLRAVPAQAPRPNRRLRKRQYR--RGHTVHSERKYVELIYINDQLF 252
OY      313  KHRSSHHTNNFAKSVNLVDSITYEQDLNTRVLVAVEFTERKQIDITTPVOMLHEF 372
DB      253  EOMROSVALTSNFAKSVNLADVLYKQDLNTRVLVAVEFTERKQIDITTPVOMLHEF 312
OY      373  SKYROR-IRQHADAHLISVTFHYKRSLSYEGVCSFRTGVNVEYGLPMAVAQLSLQ 431
DB      313  MYRRBEGLPEPSNATHLFSGRTPQSTSSGAAYVGLCSLHGGGVNFGNMKGAAVTLAQ 372
OY      432  SLAONLGIOW-EPSRRPKDCTESMGCIMEETGVSRSKRFKSCSILEYRDLQORGGA 490
DB      373  TLGONLGMNKNKRRSSAGDKCPDMLGCIIMEDTGFLPKRFSKSIDEVNQLQEGGS 432
OY      491  CLFNRPKLEFPEECGGVYEAEECCGCHVECY---GLCKCKCSLSNAGHSDGQCEN 547
DB      433  CLFNRPKLEFPEECGGVYEAEECCGCHVECY---GLCKCKCSLSNAGHSDGQCEN 492
OY      548  NTSCLFQPRGYECRDVANECDITEYCTGDSGQCPNHLKODGYACNONGRCVNGECKTR 607
DB      493  R--CYEPRGVSCREAVNECDIAETCTGDSGQCPNHLKODGYACNONGRCVNGECKTR 550
OY      608  DMCQOYIWGTRKAAGSDKFCYEKLNTEGTEKNGCKGKDDRMWIOCKSHDVFPGFLLCTNLTJR 667
DB      551  DRQCVLWGHAAA--DRECYEKLNVGTERGSRKSGMVGQCSKQDVLGCFLLCVNLSG 608
OY      668  APRIGOLGELIPTSFYHOGRAVIDCSGAHVLLDDPDVGVVEGTGPGSPMMLCDRCLQ 727
DB      609  APRIGDLVGDIISSVTFYHOGKEIDCRGHVQLAGSDLSYEDDTAGCPNMLCIDHRCPL 668
OY      728  IQALNMSGCLPSDKGKVCSGHGVCSNEATCICDFTTAGTDCSIRDPVRLNHPK--KDEGPK 786
DB      669  ASAPNFSTGPGSGERRICSHGVCSNECKTCLQDPMWTKGDSIINPLPTSPPTQETERYK 728
OY      787  GPSATNLIIGSIAGAILVAALVILGCTGNGFNKVR 823
DB      729  GPSGTNIIIGSIAGAILVAALVILGCTGNGFNKIRRR 765

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RESULT 3
US-08-477-407-4
: Sequence 4, Application US/08477407
: Patent No. 5631351
: GENERAL INFORMATION:
: APPLICANT: NAKAMURA, YUSUKE
: APPLICANT: EMI, MITSURU
: TITLE OF INVENTION: MDC PROTEINS AND DNAs
: TITLE OF INVENTION: ENCODING THE SAME

```



NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLYNN, THEL, BOUTELL & TANIS P.C.  
STREET: 2026 Rambling Road  
CITY: Kalamazoo  
STATE: Michigan  
COUNTRY: USA  
ZIP: 49008-1699  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage  
COMPUTER: IBM PC/XT/AT Compatible  
OPERATING SYSTEM: MS-DOS 5.0  
SOFTWARE: WordPerfect 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477, 407  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/243,542  
FILING DATE: 13-MAY-1994  
APPLICATION NUMBER: JP 5-136602  
FILING DATE: 14 MAY 1993  
APPLICATION NUMBER: JP 5-257455  
FILING DATE: 22 SEPTEMBER 1993  
APPLICATION NUMBER: JP 6-49904  
FILING DATE: 23 FEBRUARY 1994  
APPLICATION NUMBER: JP 6-73328  
FILING DATE: 12 APRIL 1994  
APPLICATION NUMBER: JP 6-84470  
FILING DATE: 22 APRIL 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Teriyence F. Chapman  
REGISTRATION NUMBER: 32 549  
REFERENCE/DOCKET NUMBER: Furuya Case 1313  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (616) 381-1156  
TELEFAX: (616) 381-5465  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 769 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
LIBRARY: human fetal brain cDNA library  
US-08-477-407-4

Query Match 43.4%; Score 1978; DB 1; Length 769;  
Best Local Similarity 48.6%; Pred. No. 5,3e-155;  
Matches 397; Conservative 93; Mismatches 225; Indels 102; Gaps 17;  
QY 46 LLLVLLLPPLAASSRRA--WGA-----AAPSAPHNNETAENKLVGLADEDNLTLOHSSS 99  
DB 12 LLLSLPPGLCTGCPAGALRWGLGPGAP----- 45  
QY 100 NISYSNAMOKEITLPSRLIYIYNODESPYHYLDTKARHQKKNKAVHLAQAQFOIEAFG 159  
DB 46 -----EYTESRLVRE--SSGGEVKKOOLDTRVROEPGPGPVHLLQVSFVDAFM 94  
QY 160 SKFILDILNGLSSDYVEIHY-ENGKPOYSKG-GEHCYHGSIRGVDSKVALS:YCNQ 217  
DB 95 SNFTLDLELNHLLSSQYVERHFSRGTQHSYGAGDHCYCGKLGKNGHPSFALS:YCGG 154  
QY 218 LHGMEDDTFVYMIPLLEV--HDEKSTORPHIQTTLGQYSKQKNLTMERGDQPL 275  
DB 155 LHGVSDGDLTYIVEQEVAGPWPAGPQPLPHLYRT-----PLI 194  
QY 276 SELQWLK-----RRKRVNPSRG---IPEEMKYLEIMLVNDHKTY 312  
DB 195 PPLGCRPGCLFANVPAOSAPPNRRLRKKROYR--RGHPYHSETKYVELIVINDHQLP 252

QY 313 KKRSSHAFNNFNFAKSVVNLVDSIYKBOILNTRVVLVAVETWTEKDOIITNNPYQMLHEF 372  
DB 253 EQMHQSVLNLNFAKSVVNLADVIYKBOILNTRIVLVAMETWADBDKIQVQDDLETYARL 312  
QY 373 SKYROR-IKOHADAVHLISRTVTHYKRSLSLFEQVCSRTRGVNEYGLPMAVAQVLSQ 431  
DB 313 MYVRREGLPEPSNATHLFSGRTPPOSTSSGAAYVGGICSLSHGGGVNEYGNMGAMAVTLAQ 372  
QY 432 SLQONIGIOW-EPSRRPKDCCTESMGCITHEEFGVSHSRKFSKSTILEYDOLFQRGGA 490  
DB 373 TLGONLGMNMMKRRSSAGDCKCPDMLGCIHEDYFLPRKFSRCSIDENYQFLQEGGS 432  
QY 491 CLEFRPKLEPTEPCGNGYVAGEECDCGFHVECY---GLCCRKSLSNGAHSDBGPCN 547  
DB 433 CLFRNPKPLKLDPPCGNGFVAGEECDCGSVQESRAGNCKCKCTLPHDMACSDGLCCR 492  
QY 548 NTSCLFPQRGYECRDVANECDITHEYCTGDSGQCPNHLKODGYACNONGRCYNECKTR 607  
DB 493 R--CKYEPRGVSGCREAVNECDIAETCTGDSGQCPNHLKLDGYCDHEDGRCYGRCKTR 550  
QY 608 DNOQYIWTGTRKAGSDKFCYEKLTETGTEKNGCKGKDDRWITQSKHDVFCGFLCTLNLR 667  
DB 551 DRQCVLMGHAA--DRFCTEKLVEGTERSCGRKSGMWQCSKQDVLGFLICLVNTS 608  
QY 668 APRIGLOGELIIPSYFHOGRVIDCSGAVVLDDBTVDYGVYEDTGPCPSMCKLDRKCLQ 727  
DB 609 APRIGDLVGDISSVTFYHOGKELDCRGHVGLAGSDLSYEDDTACGPNMLCLDHRCPL 668  
QY 728 IQALNMSSCPIDSKGKVCSGHGVCSNEATYCTCDFTWAGTDCSINDPVANLHP--KDEGPK 786  
DB 669 ASAFNFSTCPGSGGERRICSHHGVCNSNEKCICQPDWKGKDCSINHPLPTSPPTGETERYK 728  
QY 787 GPSATNLISAGAILVAALVILGTMGFANVKKR 823  
DB 729 GPSGTNIIIGSIAGVLAALVILGTMGFENIRGR 765

## RESULT 4

US-08-484-355-4:  
Sequence 4, Application US/08484355  
Patent No. 5705341  
GENERAL INFORMATION:  
APPLICANT: NAKAMURA, YUSUKE  
TITLE OF INVENTION: MDC PROTEINS AND DNAS  
TITLE OF INVENTION: ENCODING THE SAME  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLYNN, THEL, BOUTELL & TANIS P.C.  
STREET: 2026 Rambling Road  
CITY: Kalamazoo  
STATE: Michigan  
COUNTRY: USA  
ZIP: 49008-1699  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage  
COMPUTER: IBM PC/XT/AT Compatible  
OPERATING SYSTEM: MS-DOS 5.0  
SOFTWARE: WordPerfect 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484, 355  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/243, 542  
FILING DATE: 13-MAY-1994  
APPLICATION NUMBER: JP 5-136602  
FILING DATE: 14 MAY 1993  
APPLICATION NUMBER: JP 5-257455  
FILING DATE: 22 SEPTEMBER 1993  
APPLICATION NUMBER: JP 6-49904  
FILING DATE: 23 FEBRUARY 1994  
APPLICATION NUMBER: JP 6-73328

```

: FILING DATE: 12 APRIL 1994
: APPLICATION NUMBER: JP 6-84470
: FILING DATE: 22 APRIL 1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Terrence F. Chapman
: REGISTRATION NUMBER: 32 549
: REFERENCE/DOCKET NUMBER: Furuya Case 1313
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (616) 381-1156
: TELEFAX: (616) 381-5465
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 769 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: IMMEDIATE SOURCE:
: LIBRARY: human fetal brain cDNA library
: US-08-484-355-4

```

Query Match 43.4%; Score 1978; DB 1; Length 769;

Best Local Similarity 48.6%; Pred. No. 5,3e-155; Mismatches 225; Indels 102; Gaps 17;

```

Matches 397; Conservative 93; Mismatches 225; Indels 102; Gaps 17;

: 46 LLLVLLLPPLAASSRRA--WGA---AAPSAPHWNETAEKNLGLVADEDNLTLOQSSS 99
: 12 LLLSLPTGTLTGCPAGALRWGGLPOLGPGAP----- 45
: 100 NISYSNAAKETTLPRLIYINODESEYHVDTCARHQKINKNAVHLAQAFOIEARG 159
: 46 -----EYEPRLVRE--SSGGEVRKQQLDTRVROEPGPGPVHLAQAQSEVPAFN 94
: 160 SKFIIDLINGLSSDYVEIHH--ENGKPOYSKG--GEHCYHGSIRGVKSKYALSTCNG 217
: 95 SNFTDLLELNHLSSQYVERHRSREGTQHSAGADHCYQGLKNGNPSFALSTCQ 154
: 218 LHMFEEDTFYVYIPELEV--HDEKSTGRPHIIOKTLAGQYSOKMKNLTMERGDMPL 275
: 155 LHGVFSDGNLIYIVEPOEYAVGAPGAPGRLPHLIVRT-----PLL 194
: 276 SELQNLK-----RRKRAVNPGRG---IPEKKYLEMTVNDHKTY 312
: 195 PDLGREGGCLFAVAQAAPRPRRLRRKROYR--RGHPTVASEIKYVLLIYNHQLF 252
: 313 KHRSSHAHTNNEFAKSVNLVDSIYKEQLNTRVLAVAETWTEKQDITTPNVOMLHEF 372
: 253 EOMROSIVLTSNFAKSVNLADVIYKEQLNTRIVLAMETWADGDKIOVODDLLETARL 312
: 373 SKYROR--IQOHDAVHLISRVPHYKRSSLSTYFGVCSRTRGVGVNVEYGLPMAVAQVLSQ 431
: 313 MYVRREGLEPSNATLFGSRFTOSTSSGAAYVGICSLSHGGVNEYGMGMAAYTLAQ 372
: 432 SLAONLGIOM--EPSSRRPKCDCTESWGCI MEETGSHSRKFSKSTLEFRDLQSGGA 490
: 373 TLGONLGMAMNKHRSASGCKPCDILWLCIMETGYLPLPKFSCSIDENQLOBEGGS 432
: 491 CLFNRPKLPTEPECNGIYAGEECDCGFHVECY---GLCKCKSLSNAGHCSDPCCN 547
: 433 CLFNKPLKLLDPECCNGFEAGEECDCGSGVQCSRAAGCNCKKCTLLHDAMCSDGICCR 492
: 548 NTSCLFOPRGYECRDVAVNECDITEYCTGDSGQCPRLNHRKQDYAACNORCNGECKTR 607
: 493 R--CKTEPRVSCREAVNECDIAETCTGDSQCPRLNHRKQDYAACNORCNGECKTR 550
: 608 DNOCYITWGTAKAGSKFCYEKLNTEGTEKNGCKGDQDRAIQSCSHDVFEGFLCTMLTR 667
: 551 DRCCYVLMGMAA--DRFCYEKLNTEGTEKNGCKGSGVQCSKQDYVLCGFLICVNISSG 608
: 668 APRIGOLGEIITPSTYHOGRIYDCSGAHVYLDLDDTVGVYEDGTGCGPSMCLDRKCLQ 727
: 609 APRGLDVGDISSVTFYHOGKEIKDCRGHVALDAGSDLSVYEDGTAGCPMMLCIDHRCPL 668

```

```

: 728 IQALNNSCPDLSKRGVCSGHGVCSEATCIDEFTWAGTIDCSTRDVRNLHP--KDEGRK 786
: 669 ASAFNSTCPGSEERRICSHHGVCSNECKICOPDWTGDKDCSTHNLPTSPPTGETERYK 728
: 787 GPSATMLIGSTAGALVAALVYLGTCWGFKNKKRR 823
: 729 GPSGTMIIGSTAGALVAALVYLGTCWGFKNIRGR 765

```

#### RESULT 5

US-08-243-542-3

```

: Sequence 3, Application US/08243542
: Patent No. 5352526
: GENERAL INFORMATION:
: APPLICANT: NAKAMURA, YOSUKE
: APPLICANT: EMI, MITSURU
: TITLE OF INVENTION: MDC PROTEINS AND DNAs
: TITLE OF INVENTION: ENCODING THE SAME
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
: STREET: 2026 Rambling Road
: CITY: Kalamazoo
: STATE: Michigan
: COUNTRY: USA
: ZIP: 49008-1699

```

#### COMPUTER READABLE FORM:

```

: MEDIUM TYPE: Diskette, 3.5 inches, 1.44 MB storage
: COMPUTER: IBM PC/XT/AT Compatible
: OPERATING SYSTEM: MS-DOS 5.0
: SOFTWARE: WordPerfect 5.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/243,542
: FILING DATE:
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 5-136602

```

```

: FILING DATE: 14 MAY 1993
: APPLICATION NUMBER: JP 5-257455
: FILING DATE: 22 SEPTEMBER 1993
: APPLICATION NUMBER: JP 6-49904
: FILING DATE: 23 FEBRUARY 1994
: APPLICATION NUMBER: JP 6-73328
: FILING DATE: 12 APRIL 1994
: APPLICATION NUMBER: JP 6-84470

```

```

: FILING DATE: 22 APRIL 1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Terrence F. Chapman
: REGISTRATION NUMBER: 32 549
: REFERENCE/DOCKET NUMBER: Furuya Case 1313
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (616) 381-1156
: TELEFAX: (616) 381-5465
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 670 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: IMMEDIATE SOURCE:
: LIBRARY: human fetal brain cDNA library
: US-08-243-542-3

```

Query Match 41.0%; Score 1867.5; DB 1; Length 670;

Best Local Similarity 51.8%; Pred. No. 6e-146; Mismatches 184; Indels 59; Gaps 13;

```

Matches 357; Conservative 89; Mismatches 184; Indels 59; Gaps 13;

: 168 LNNGLSSDYVEIHH--ENGKPOYSKG--GEHCYHGSIRGVKDSKVALSTCNGLHMGFEED 225
: 4 LSHOLSSQYVERHRSREGTQHSAGADHCYQGLKNGNPSFALSTCQGLHGVSDG 63

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Db 518 GDISSVTFYHQGKELDCRGHVOLADSDLSYEDGTACGPNMLCDHRCLPASAFNFST 577  
OY 736 CPLDSKRGVCSGHGVCNEATCICDFTWAGTDCSIRDPVRNLHP-KDEGFKGSATNLI 794  
Db 578 CPGSGERRICSHHGVCSNEKGCICOPDWTGKDCSIHNLPLSPPTGETERYKGPSTGNTII 637  
OY 795 IGSTAGAILVAIYVIGTGWGFKNVKKRR 823  
Db 638 IGSTAGAVLAIAIYVIGTGWGFKNIRRR 666

## RESULT 7

US-08-484-355-3  
Sequence 3, Application US/08484355  
Patent No. 5705341

## GENERAL INFORMATION:

APPLICANT: NAKAMURA, YUSUKE  
APPLICANT: EMI, MITSURU  
TITLE OF INVENTION: MDC PROTEINS AND DNAs  
TITLE OF INVENTION: ENCODING THE SAME  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.  
STREET: 2026 Rambling Road  
CITY: Kalamazoo  
STATE: Michigan  
COUNTRY: USA

## ZIP: 49008-1699

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage  
COMPUTER: IBM PC/XT/AT Compatible  
OPERATING SYSTEM: MS-DOS 5.0

## SOFTWARE: Wordperfect 5.0

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,355  
FILING DATE: 07-JUN-1995

## CLASSIFICATION: 536

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/243,542  
FILING DATE: 13-MAY-1994

APPLICATION NUMBER: JP 5-136602  
FILING DATE: 14 MAY 1993

APPLICATION NUMBER: JP 5-257455  
FILING DATE: 22 SEPTEMBER 1993

APPLICATION NUMBER: JP 6-49904  
FILING DATE: 23 FEBRUARY 1994

APPLICATION NUMBER: JP 6-73328  
FILING DATE: 12 APRIL 1994

APPLICATION NUMBER: JP 6-84470  
FILING DATE: 22 APRIL 1994

ATTORNEY/AGENT INFORMATION:  
NAME: Teriyence F. Chapman

REGISTRATION NUMBER: 32 549  
REFERENCE/DOCKET NUMBER: Furuya Case 1313

TELEPHONE: (616) 381-1156  
TELEFAX: (616) 381-5465

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:

LENGTH: 670 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein

ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:

LIBRARY: human fetal brain cDNA library  
US-08-484-355-3

Query Match 41.0%; Score 1867.5; DB 1; Length 670;  
Best Local Similarity 51.8%; Pred. No. 6e-146;  
Matches 357; Conservative 89; Mismatches 184; Indels 59; Gaps 13;

OY 168 LNNGLSSDYVEIHY-ENGKPOYSKG-GEHCYHSGISIRGVKDSKVALSTCNLHGFEED 225  
Db 4 LSHOLLSSQYVERHRHSRECTTOHSTAGDHCYQCKLRNPNHFAALSTCOGLHGVFSG 63  
OY 226 TFVYVIEPIELV--HDEKSTGRPHIIOKTLAQOYSOMKNLMEMGGDQPFSELOWLK- 282  
Db 64 NLTYIVEPOEVAGPMGADGPLPLHLYR-----PLLPDLGCGE 103  
OY 283 -----RRKRAVNPSSG---IFEEMKYLELMTVNDKRYKKHSSHA 320  
Db 104 PCLFAVPAQASAPPNRPRLRRKRQVR--RGHPTVHSETVVELIYINDHQLEFOMQSVV 161  
OY 321 HTNNEFAKSVNLDVSYKEQLNTRVYLVAVETWTEKDQIDITTPVQMLHESKYROR-1 379  
Db 162 LTSNFAKSVNLDVSYKEQLNTRVYLVAVETWTEKDQIDITTPVQMLHESKYROR-1 221  
OY 380 KOHDAVHLISRTFHYKRSLSYFPGVCSRTGCVNVEYGLMAVAOVLQSLAONLGI 439  
Db 222 PEPSSNATHLFSGRTFPOSTSSGAAYVGGTSLSHGGVNETGNMGAMAVYLAOTLQONLGM 281  
OY 440 QW-EPSSRRPKDCTESMGCI MEETGVSHSRKFSKSILEYRDLQORGAGCLFNRPTK 498  
Db 282 MNKHSSAGDCKCPDINLQCI MEDIGFYLPRFRSCSIDEVNOFLQEGGSCFLFNKPLK 341  
OY 499 LFEPTCGNGYVEAGECDGCFHVECY---GLCKKCSLSNGARCSDPCCNNTSCLFOP 555  
Db 342 LDPPECGNGFVAGECDGCGVQECSSRAAGNCKCKTTLTHDMCSDGLCCRR--CYEP 399  
OY 556 RGYECRDVAHECOTTECTGDSGCPNHLKODGYACNOGRCYNECKTRPNOCYIY 615  
Db 400 RGVSCRAVNECDIAECTGDSGCPNHLKODGYACNOGRCYNECKTRPNOCYIY 459  
OY 616 GTAAGSDKFCYEKLNTETGKNGCGKDGRIWIDCSKHDFECGFLCTNLTRAPRIGOLQ 675  
Db 460 GHAA--DRCYELNTEGTERGSCGRKSGMWVCCSDOVLGCLLVNISGARLDDLV 517  
OY 676 GEIIPTSFYHQGRVIDCSGAHVLLDDTDYGYVEDGTTPCGPSMMCLDRKCLQIALMSS 735  
Db 518 GDISSVTFYHQGKELDCRGHVOLADSDLSYEDGTACGPNMLCDHRCLPASAFNFST 577  
OY 736 CPLDSKRGVCSGHGVCNEATCICDFTWAGTDCSIRDPVRNLHP-KDEGFKGSATNLI 794  
Db 578 CPGSGERRICSHHGVCSNEKGCICOPDWTGKDCSIHNLPLSPPTGETERYKGPSTGNTII 637  
OY 795 IGSTAGAILVAIYVIGTGWGFKNVKKRR 823  
Db 638 IGSTAGAVLAIAIYVIGTGWGFKNIRRR 666

## RESULT 8

US-08-243-542-2  
Sequence 2, Application US/08243542  
Patent No. 5552526

## GENERAL INFORMATION:

APPLICANT: NAKAMURA, YUSUKE  
APPLICANT: EMI, MITSURU  
TITLE OF INVENTION: MDC PROTEINS AND DNAs  
TITLE OF INVENTION: ENCODING THE SAME  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.  
STREET: 2026 Rambling Road  
CITY: Kalamazoo  
STATE: Michigan  
COUNTRY: USA

## ZIP: 49008-1699

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage  
COMPUTER: IBM PC/XT/AT Compatible  
OPERATING SYSTEM: MS-DOS 5.0

## SOFTWARE: Wordperfect 5.0

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/243,542

FILED DATE: 530  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-136602  
FILING DATE: 14 MAY 1993  
APPLICATION NUMBER: JP 5-257455  
FILING DATE: 22 SEPTEMBER 1993  
APPLICATION NUMBER: JP 6-49904  
FILING DATE: 23 FEBRUARY 1994  
APPLICATION NUMBER: JP 6-73328  
FILING DATE: 12 APRIL 1994  
APPLICATION NUMBER: JP 6-84470  
FILING DATE: 22 APRIL 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Terrence F. Chapman  
REGISTRATION NUMBER: 32 549  
REFERENCE/DOCKET NUMBER: Furuya Case 1313  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (616) 381-1156  
TELEFAX: (616) 381-5465  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 524 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
LIBRARY: human fetal brain cDNA library  
US-08-243-342-2.

Query Match 28.5%; Score 1297; DB 1; Length 524;  
Best Local Similarity 49.5%; Pred. No. 6.2e-99;  
Matches 256; Conservative 65; Mismatches 138; Indels 58; Gaps 12;

168 LNLGLSSDYVEIHY-ENGKPOYSKG-GEHCYHGSIRGVKSKVALSTCGLHGFEDD 225  
4 LSHOLLSSQYVERHRSREGTTOHSTGAGDHCYOGKLRGNPHSFALSTCOGLHGFESDG 63  
226 TFEVYMIPELELV--HDEKSTGRPHIIOKTLAQSOKMKNLMERDQWFLSELQMLK- 282  
64 NLTYIVEPQVAVPAGPAPGRLPHLYRT-----PLPDPPLGCRE 103  
283 -----RRKRAVNPSRG---IFEEMKYLEIMIVNDHKTYKKHRS SHA 320  
104 PGCLFAVPAQASAPRPNRLRRKROVR--RGHPTVHSETKYVELIVINDHOLFEOQMSV 161  
321 HTNNAKSVNLVDSITYKEQLNTRVYLAVERWTEKQDIDITTPYOMLHEFSKYRQR-I 379  
162 LTSNFAKSVNLADVIYKEQLNTRIVLVMETWADGDKIOVODDLETLARLWYRREGI 221  
380 KOHADAVHLISRVTFHYKRSLSYFGVCSRTRGVNVNEXGLPMNAQVLSOSLQNLGI 439  
222 PEPNATLHLSGRTFOSTSSGAAVYGGISLHGGVNVYGMNMAVTLAOTLQNLGM 281  
440 QW-EPPSRKPKDCCTESWGCGIMEETGVSHSRKFKCSILEYRDFLORGAGCLEFNRPTK 498  
282 MNKHRSSAGDCKCPDMLGCMEDTGFYLPKRFSCSIDENQFLQDEGSGCLFNRPLK 341  
499 LPEPPECNGYVEAGEEDCCGFHVICY---GLCKKCSLSNAGHSGDGFCCNNTSCLFOP 555  
342 LLDPEPCNGYVEAGEEDCCGVQCSFRAGCNCKCTLTLDHAMSGLCCRR--CKYEP 399  
556 RGYECRDVAVNECDITREYCTGDSGOCPPNLRKQDGYACNOCRCVNGECKTDNOCQYIM 615  
400 RGVSRERAVNECDIAETCTGDSGOCPPNLRKQDGYACNOCRCVNGECKTDNOCQYIM 459  
616 GTKAAGSDKFCYEKLNTEKTEKNGCNCKDGRWITQSC 652  
460 GHAAL--DRFCYEKLNTEKTEKNGCNCKDGRWITQSC 494

RESULT 9  
US-08-477-407-2  
Sequence 2, Application US/08477407  
Patent No. 5631351  
GENERAL INFORMATION:  
APPLICANT: NAKAMURA, YUSUKE  
APPLICANT: EMI, MITSURU  
TITLE OF INVENTION: MDC PROTEINS AND DNAs  
TITLE OF INVENTION: ENCODING THE SAME  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.  
STREET: 2026 Rambling Road  
City: Kalamazoo  
STATE: Michigan  
COUNTRY: USA  
ZIP: 49008-1699  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage  
COMPUTER: IBM PC/XT/AT Compatible  
OPERATING SYSTEM: MS-DOS 5.0  
SOFTWARE: Wordperfect 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,407  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/243,542  
FILING DATE: 13-MAY-1994  
APPLICATION NUMBER: JP 5-136602  
FILING DATE: 14 MAY 1993  
APPLICATION NUMBER: JP 5-257455  
FILING DATE: 22 SEPTEMBER 1993  
APPLICATION NUMBER: JP 6-49904  
FILING DATE: 23 FEBRUARY 1994  
APPLICATION NUMBER: JP 6-73328  
FILING DATE: 12 APRIL 1994  
APPLICATION NUMBER: JP 6-84470  
FILING DATE: 22 APRIL 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Terrence F. Chapman  
REGISTRATION NUMBER: 32 549  
REFERENCE/DOCKET NUMBER: Furuya Case 1313  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (616) 381-1156  
TELEFAX: (616) 381-5465  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 524 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
LIBRARY: human fetal brain cDNA library  
US-08-477-407-2

Query Match 28.5%; Score 1297; DB 1; Length 524;  
Best Local Similarity 49.5%; Pred. No. 6.2e-99;  
Matches 256; Conservative 65; Mismatches 138; Indels 58; Gaps 12;

168 LNLGLSSDYVEIHY-ENGKPOYSKG-GEHCYHGSIRGVKSKVALSTCGLHGFEDD 225  
4 LSHOLLSSQYVERHRSREGTTOHSTGAGDHCYOGKLRGNPHSFALSTCOGLHGFESDG 63  
226 TFEVYMIPELELV--HDEKSTGRPHIIOKTLAQSOKMKNLMERDQWFLSELQMLK- 282  
64 NLTYIVEPQVAVPAGPAPGRLPHLYRT-----PLPDPPLGCRE 103  
283 -----RRKRAVNPSRG---IFEEMKYLEIMIVNDHKTYKKHRS SHA 320  
104 PGCLFAVPAQASAPRPNRLRRKROVR--RGHPTVHSETKYVELIVINDHOLFEOQMSV 161

```

OY 321 HTNNFAKSVNLDVSYKEDLNTRVYLVAVETWTEKQDIDITTPVOMLHEFSKYRQ-R-I 379
Db 162 LTNFPAKSVNLDVYIKEDLNTRIVYLVAVETWADGKIYOVDLLETFLARLWVYREG-L 221
OY 380 KOHADAVHLISRYTFLHKKSSLSYFGVCSRTGCVNEXGLPMAVAQVLSQSLAQNIG-I 439
Db 222 PEPNATHLFSGRFTPOSTSSGAAYVGCISLSHGGVNEYNMAMAVTLAOTLGONLGM 281
OY 440 QW-EPSRRKPKCDCTESMGCCIMETGVSHSRKFSKSLIERYDFLORGAGCLFNRPTK 498
Db 282 MMKHKRSAGDCKCPDILMCGIMEDTGFYLPKRFSRCSIDENQFLOEGGSCLEFNKPLK 341
OY 499 LFEPTGNGVYVAGEECDCGFHVECY--GLCCCKCSLSNGAHCSDGPCCNNTSCLFOP 555
Db 342 LLDPECGNGFVEAGEECDCGVQECSSRAGNCCCKCTLTLDAMCSDGLCCR--CKYEP 399
OY 556 RGYECRDVAVNECDITTEYCTDGGCCPPNHLKODGYACNONOGRVNGECKTRDNOCOYI-W 615
Db 400 RGVSCREAVNECDIAETCTGDSGCCPPNHLKLDGYCHDEGRGCGYGRCKTRDNOCOYI-W 459
OY 616 GTKAAGSDKRCYKLTNEGTEKNGCGKDGDRWIOCSK 652
Db 460 GHAAA--DRFCYKLVNEGTERGSCGRKSGWVQCSK 494

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RESULT 10
US-08-484-355-2
; Sequence 2, Application US/08484355
; Patent No. 5705341
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, YUSUKE
; APPLICANT: EMI, MITSURU
; TITLE OF INVENTION: MDC PROTEINS AND DNAS
; TITLE OF INVENTION: ENCODING THE SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSER: FLYNN, THEIL, BOUTELL & TANIS P.C.
; STREET: 2026 Rambling Road
; CITY: Kalamazoo
; STATE: Michigan
; COUNTRY: USA
; ZIP: 49008-1699
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inches, 1.44 MB storage
; OPERATING SYSTEM: MS-DOS 5.0
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,355
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/243,542
; FILING DATE: 13-MAY-1994
; APPLICATION NUMBER: JP 5-136602
; FILING DATE: 14 MAY 1993
; APPLICATION NUMBER: JP 5-257455
; FILING DATE: 22 SEPTEMBER 1993
; APPLICATION NUMBER: JP 6-49904
; FILING DATE: 23 FEBRUARY 1994
; APPLICATION NUMBER: JP 6-73328
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: JP 6-44470
; FILING DATE: 22 APRIL 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Terrence F. Chapman
; REGISTRATION NUMBER: 32 549
; REFERENCE/DOCKET NUMBER: Furuya Case 1313
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (616) 381-1156
; TELEFAX: (616) 381-5465
; INFORMATION FOR SEQ ID NO: 2:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 524 amino acids
; TYPE: amino acid
; TOPOLOGY: Linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; LIBRARY: human fetal brain cDNA library
US-08-484-355-2

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Query Match 28.5%; Score 1297; DB 1; Length 524;
Best Local Similarity 49.5%; Pred. No. 6, 2e-99;
Matches 256; Conservativity 65; Mismatches 136; Indels 58; Gaps 12;

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OY 168 LNNGLSSDYVEIHY-ENGKPKQYSG-GEHCYHGSIRGVNDSKVALSTONGLHGMFEDD 225
Db 4 LSHQLLSSQYVYRHSRETTQHSAGAGHCYQKRLBNPSPFALSTCQSLHGVFSDG 63
OY 226 TFVYVIEPLELY--HDEKSTGRPHIIOKTLAQOYSKQKNLTMERGDQWPFISLQWLK- 282
Db 64 NLTYIYEPQEVAGPWCAPQGPPLPHLYRT-----PLLPDPLGCRE 103
OY 283 -----RRKRAVNSRG-----IFEMKYLELMIYNDKTKYKRRSSHA 320
Db 104 PGCLFAVPAQSAAPPNPRLLRRKQYR--RGHPVHSETYVELIYINDHQLFQMRQSYV 161
OY 321 HTNNFAKSVNLDVSYKEDLNTRVYLVAVETWTEKQDIDITTPVOMLHEFSKYRQ-R-I 379
Db 162 LTNFPAKSVNLDVYIKEDLNTRIVYLVAVETWADGKIYOVDLLETFLARLWVYREG-L 221
OY 380 KOHADAVHLISRYTFLHKKSSLSYFGVCSRTGCVNEXGLPMAVAQVLSQSLAQNIG-I 439
Db 222 PEPNATHLFSGRFTPOSTSSGAAYVGCISLSHGGVNEYNMAMAVTLAOTLGONLGM 281
OY 440 QW-EPSRRKPKCDCTESMGCCIMETGVSHSRKFSKSLIERYDFLORGAGCLFNRPTK 498
Db 282 MMKHKRSAGDCKCPDILMCGIMEDTGFYLPKRFSRCSIDENQFLOEGGSCLEFNKPLK 341
OY 499 LFEPTGNGVYVAGEECDCGFHVECY--GLCCCKCSLSNGAHCSDGPCCNNTSCLFOP 555
Db 342 LLDPECGNGFVEAGEECDCGVQECSSRAGNCCCKCTLTLDAMCSDGLCCR--CKYEP 399
OY 556 RGYECRDVAVNECDITTEYCTDGGCCPPNHLKODGYACNONOGRVNGECKTRDNOCOYI-W 615
Db 400 RGVSCREAVNECDIAETCTGDSGCCPPNHLKLDGYCHDEGRGCGYGRCKTRDNOCOYI-W 459
OY 616 GTKAAGSDKRCYKLTNEGTEKNGCGKDGDRWIOCSK 652
Db 460 GHAAA--DRFCYKLVNEGTERGSCGRKSGWVQCSK 494

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RESULT 11
US-08-243-542-1
; Sequence 1, Application US/08243542
; Patent No. 5552526
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, YUSUKE
; APPLICANT: EMI, MITSURU
; TITLE OF INVENTION: MDC PROTEINS AND DNAS
; TITLE OF INVENTION: ENCODING THE SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSER: FLYNN, THEIL, BOUTELL & TANIS P.C.
; STREET: 2026 Rambling Road
; CITY: Kalamazoo
; STATE: Michigan
; COUNTRY: USA
; ZIP: 49008-1699
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inches, 1.44 MB storage
; OPERATING SYSTEM: MS-DOS 5.0

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OY 283 -----RRKRAVPSRG---IFEEMKYLEMTVNDHKTYKKHRS SHAHTNN 324
Db 101 FAVPAQSA PPRPRRRKROYR--RGHPYHSETKYVELIVINDHQLFEOMROSVLITSN 158
OY 325 FAKSVNVLVDISIYKEQLNTRVVLVAVETWTEKDQIDITTPVQMLHEFSKYROR- IKOHA 383
Db 159 FAKSVNVLADVIYKQQLNTRIVLVMETWADGDKIQVODDLETLARLMLVYRREGLEPES 218
OY 384 DAVHLISRVTTHYKRSSLSTYFGVCSRTRGVGVNEYGLPMAVAQVLSOSLAONLGIOW-E 442
Db 219 NATHLFSGRTOFSTSSGAAYVGGICLSHGGGVNEYGNMGAMAVTLAOTLGNLGMNMNK 278
OY 443 PSRRPKCDCTESMGCIMETGVSHSRFSKCSILEYRDFLORGGACLFNRPTRLEP 502
Db 279 HRSSAGDCKCPDIWLGCTIMEDTGFYLPKRFSCSIDETYNQFLOEGGSGCLFNKPLKIDP 338
OY 503 TECNGVYEAGEECDGCFHVECY---GLCKKCSLSNGAHCSDGPCCNTNTSCLFOPRGYE 559
Db 339 PECGNGFEVAGEECDGSGVQECSSRAGNCKKCTLHDAMCSDGLCCRR--CKYEDRGVS 396
OY 560 CRDAVNECDITEYCTGDSGQCPNHLKODGYACNONOGRCYNGECKTRDNOCCOYIMGTKA 619
Db 397 CREAVNECDIAETCTGDSQCPNHLKLDGYCDHEOGRCYGRCRTDRDCCOVLWGHAA 456
OY 620 AGSDKECYEXTTEGTEKNGCGKDGDRWTQCSK 652
Db 457 A--DRECYEKLNVESTERGSGRGSGWVQCSK 487

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Search completed: June 1, 2003, 18:34:56  
 Job time : 59 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2003, 18:30:26 ; Search time 128 seconds  
(without alignments)  
657.954 Million cell updates/sec

Title: US-09-634-252a-4  
Perfect score: 4553  
Sequence: 1 MKPPGSSSRQPLAGCSLAG.....GNGFKNVKRRRDPDTPQGP 832

Scoring table: BIOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

**Published Applications AA..\***  
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2: /cgn2\_6/ptodata/1/pubpaa/PCR\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
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9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
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11: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4553	100.0	832	US-09-824-129-3	Sequence 3, Appl 1
2	3621	79.5	696	US-09-809-790-2	Sequence 2, Appl 1
3	3621	79.5	696	US-09-809-617-2	Sequence 2, Appl 1
4	1680	36.9	540	US-09-792-2008-18	Sequence 18, Appl 1
5	1007.5	22.1	778	US-10-125-470-16	Sequence 16, Appl 1
6	1007.5	22.1	778	US-10-125-452-16	Sequence 16, Appl 1
7	1007.5	22.1	778	US-09-955-504-16	Sequence 16, Appl 1
8	1007.5	22.1	918	US-10-020-733-4	Sequence 4, Appl 1
9	1007.5	22.1	918	US-10-125-470-9	Sequence 9, Appl 1
10	1007.5	22.1	918	US-10-125-452-9	Sequence 9, Appl 1
11	1007.5	22.1	918	US-09-955-504-9	Sequence 9, Appl 1
12	1007.5	22.1	926	US-10-020-733-2	Sequence 2, Appl 1
13	1007.5	22.1	955	US-10-020-733-8	Sequence 8, Appl 1
14	1007.5	22.1	963	US-10-020-733-6	Sequence 6, Appl 1
15	982	21.6	920	US-09-792-2008-16	Sequence 16, Appl 1
16	968	21.3	920	US-09-983-531A-4	Sequence 4, Appl 1
17	966	21.2	903	US-09-983-531A-2	Sequence 2, Appl 1
18	962.5	21.1	735	US-09-978-189A-74	Sequence 74, Appl 1
19	962.5	21.1	735	US-09-978-697-74	Sequence 74, Appl 1

20	962.5	21.1	735	US-09-978-192A-74	Sequence 74, Appl 1
21	962.5	21.1	735	US-09-999-832A-74	Sequence 74, Appl 1
22	962.5	21.1	735	US-09-978-189-74	Sequence 74, Appl 1
23	962.5	21.1	735	US-10-174-590-88	Sequence 88, Appl 1
24	962.5	21.1	735	US-10-176-758-88	Sequence 88, Appl 1
25	962.5	21.1	735	US-10-175-737-88	Sequence 88, Appl 1
26	962.5	21.1	735	US-10-173-706-88	Sequence 88, Appl 1
27	962.5	21.1	735	US-10-175-738-88	Sequence 88, Appl 1
28	962.5	21.1	735	US-10-175-752-88	Sequence 88, Appl 1
29	962.5	21.1	735	US-10-176-482-88	Sequence 88, Appl 1
30	962.5	21.1	735	US-10-176-757-88	Sequence 88, Appl 1
31	962.5	21.1	735	US-10-176-913-88	Sequence 88, Appl 1
32	962.5	21.1	735	US-10-180-552-88	Sequence 88, Appl 1
33	962.5	21.1	735	US-10-180-557-88	Sequence 88, Appl 1
34	962.5	21.1	735	US-10-173-700-88	Sequence 88, Appl 1
35	962.5	21.1	735	US-10-174-572-88	Sequence 88, Appl 1
36	962.5	21.1	735	US-10-174-579-88	Sequence 88, Appl 1
37	962.5	21.1	735	US-10-174-582-88	Sequence 88, Appl 1
38	962.5	21.1	735	US-10-174-588-88	Sequence 88, Appl 1
39	962.5	21.1	735	US-10-175-739-88	Sequence 88, Appl 1
40	962.5	21.1	735	US-10-175-740-88	Sequence 88, Appl 1
41	962.5	21.1	735	US-10-176-488-88	Sequence 88, Appl 1
42	962.5	21.1	735	US-10-176-492-88	Sequence 88, Appl 1
43	962.5	21.1	735	US-10-176-747-88	Sequence 88, Appl 1
44	962.5	21.1	735	US-10-176-750-88	Sequence 88, Appl 1
45	962.5	21.1	735	US-10-176-750-88	Sequence 88, Appl 1

#### ALIGNMENTS

RESULT 1  
US-09-824-129-3  
Sequence 3, Application US/09824129  
Patent No. US2002001840A1  
GENERAL INFORMATION:  
APPLICANT: Lopez-Otin, Carlos  
APPLICANT: Miguel, Santiago Cal  
APPLICANT: Freije, Jose Maria Perez  
APPLICANT: Garcia, Jose Manuel Lopez  
APPLICANT: Blanchi, Albert Bernard  
APPLICANT: Trill, Pamela  
TITLE OF INVENTION: Methods and Compositions for Modulating  
Integrin-mediated Cell-Cell Interactions  
FILE REFERENCE: D0015-NP  
CURRENT APPLICATION NUMBER: US/09/824,129  
CURRENT FILING DATE: 2001-04-02  
PRIOR APPLICATION NUMBER: 60/194,164  
PRIOR FILING DATE: 2000-04-03  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 3  
LENGTH: 832  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-824-129-3

Query Match 100.0%; Score 4553; DB 10; Length 832;  
Best Local Similarity 100.0%; Pred. No. 9.6e-301;  
Matches 832; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKPPGSSSRQPLAGCSLAGSCGPGAGVPASAPARTPPCRLLVLLPLLAAS 60  
|||||  
DB 1 MKPPGSSSRQPLAGCSLAGSCGPGAGVPASAPARTPPCRLLVLLPLLAAS 60  
|||||  
QY 61 RPRAMGAAPASAPAHMETAEKNLGVLADEDNLTQONSSNITSYNNMOKETPLPSRLIY 120  
61 RPRAMGAAPASAPAHMETAEKNLGVLADEDNLTQONSSNITSYNNMOKETPLPSRLIY 120  
|||||  
QY 121 INDESSPHVLDTKARHQCKHKKAVHQAASQIEAFSGKFTLLDILNGLSSDYVEI 180  
121 INDESSPHVLDTKARHQCKHKKAVHQAASQIEAFSGKFTLLDILNGLSSDYVEI 180  
|||||  
DB 121 INDESSPHVLDTKARHQCKHKKAVHQAASQIEAFSGKFTLLDILNGLSSDYVEI 180  
121 INDESSPHVLDTKARHQCKHKKAVHQAASQIEAFSGKFTLLDILNGLSSDYVEI 180  
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Qy	181	AH	ENCKPOXSKGCEHYXGSTRGVNDSKVALSTCGNLGMEFDDTFVYMIIEPLELVHDE	240
Db	181	HN	ENKAP0YSKSGEHYHGSIRGVNDSKVALSTCGNLGMEFDDTFVYMIIEPLELVHDE	240
Qy	241	KSTGRPHII	OKTLAGYKSKOMKNTLJMERDQMPFSELOMKRRKRAVNPSSRIIEPEMKY	300
Db	241	KSTGRPHII	OKTLAGYKSKOMKNTLJMERDQMPFSELOMKRRKRAVNPSSRIIEPEMKY	300
Qy	301	LELMIVN	HKTKYKKHRRSSHAHTNNPAKSVYLVDSITYKEQLNTRVVLVAEVTWERKDQID	360
Db	301	LELMIVN	HKTKYKKHRRSSHAHTNNPAKSVYLVDSITYKEQLNTRVVLVAEVTWERKDQID	360
Qy	361	ITTN	EVOMLHEPSKYRORIKOHADAVHLISRYTFHFKRRSLSYFGGVCSTRGVGNEYG	420
Db	361	ITTN	EVOMLHEPSKYRORIKOHADAVHLISRYTFHFKRRSLSYFGGVCSTRGVGNEYG	420
Qy	421	LPMAVAOYLS	SOSLAONLGIQWEPSSRKPCKDCOTESGCGIMEETGVSHSRKFSKCSILEY	480
Db	421	LPMAVAOYLS	SOSLAONLGIQWEPSSRKPCKDCOTESGCGIMEETGVSHSRKFSKCSILEY	480
Qy	481	RDFLORG	GACLEFNBPYKLFEPTECGNGVYEAEGECDFHNECYGLCKCKKSLSGAHC	540
Db	481	RDFLORG	GACLEFNBPYKLFEPTECGNGVYEAEGECDFHNECYGLCKCKKSLSGAHC	540
Qy	541	SDGPCNN	NTSCLEFORGYECRAVNECDITTEYCTDSDGCPPNLHKODGYACNONGRCY	600
Db	541	SDGPCNN	NTSCLEFORGYECRAVNECDITTEYCTDSDGCPPNLHKODGYACNONGRCY	600
Qy	601	NGECKTR	NOCQYINGTRKAAGSDKCYEKLNTEGTEKNGCKGKDGDRWIDCSKHDVFCGL	660
Db	601	NGECKTR	NOCQYINGTRKAAGSDKCYEKLNTEGTEKNGCKGKDGDRWIDCSKHDVFCGL	660
Qy	661	LCTN	TRAPRIGOLGELIPTPSFYHQGRVIDCSGAHVVLDDPTDVGVEYEDGTPCGPSMMC	720
Db	661	LCTN	TRAPRIGOLGELIPTPSFYHQGRVIDCSGAHVVLDDPTDVGVEYEDGTPCGPSMMC	720
Qy	721	LDRKCLQ	IQALNMSSCPLDSKGVCSGSHGVCSENAETICIDFTWAGTDCSIRDPVNRNLHP	780
Db	721	LDRKCLQ	IQALNMSSCPLDSKGVCSGSHGVCSENAETICIDFTWAGTDCSIRDPVNRNLHP	780
Qy	781	KDEBP	KGSATNLIIGSIAGAILVAAYIVLGGTGMCFKVVKKRRRDPYQGP1 832	
Db	781	KDEBP	KGSATNLIIGSIAGAILVAAYIVLGGTGMCFKVVKKRRRDPYQGP1 832	
RESULT 2				
US-09-809-790-2				
Sequence 2, Application US/09809790				
Patent No. US200220072102A1				
GENERAL INFORMATION:				
APPLICANT: Sheppard, Paul O.				
APPLICANT: Baidnur, Nand				
APPLICANT: Delscher, Theresa A.				
APPLICANT: Bishop, Paul D.				
TITLE OF INVENTION: DISINTEGRIN HOMOLOG				
FILE REFERENCE: 98-29				
CURRENT APPLICATION NUMBER: US/09/809,790				
PRIOR APPLICATION NUMBER: 2001-03-16				
PRIOR FILING DATE: 1999-07-09				
NUMBER OF SEQ ID NOS: 13				
SOFTWARE: FastSeq for Windows Version 3.0				
SEQ ID NO 2				
LENGTH: 696				
TYPE: PR1				
ORGANISM: Homo sapiens				
US-09-809-790-2				

Query Match	79.5%	Score 3621	DB 10	Length 696
Best Local Similarity	99.7%	Pred. No. 1.3e-237		
Matches 654	Conservative 0	Mismatches 2	Indels 0	Gaps 0

Dd	9	LDTKAHQCKHNKAVHLAQASFQIEAFGSFIDILLNNGLSSDVAIEIHENKPKYISK	68
QY	192	GGEHYHGSIRGVKDSKVALSTCNGIAGNEEDTFVYMIPELVEHDEKSTGRPHIOK	251
Dd	69	GGEHCHYHGSIRGVKDSKVALSTCNGIAGNEEDTFVYMIPELVEHDEKSTGRPHIOK	128
QY	252	TLAGQYSKQKMLTMRGDQMPLESLQMKRRKRAVNPBRGTFEEMKYLELMVNDHKT	311
Dd	129	TLAGQYSKQKMLTMRGDQMPLESLQMKRRKRAVNPBRGTFEEMKYLELMVNDHKT	188
QY	312	YKHRSSHATNNFAKSVNLVDSIYKEOLNTRVLAVALVTWKEQDIDITTPNVQMIHE	371
Dd	189	YKHRSSHATNNFAKSVNLVDSIYKEOLNTRVLAVALVTWKEQDIDITTPNVQMIHE	248
QY	372	FSKYRRIQOHDAVHLISRVTFHYKRSSLSTYRGVCSRFGRGVNVEYGLPMAVAQVLSQ	431
Dd	249	FSKYRRIQOHDAVHLISRVTFHYKRSSLSTYRGVCSRFGRGVNVEYGLPMAVAQVLSQ	308
QY	432	SLAQNGLIGIOWEPSRRPKCDCTESMGCI MEETGVSHSRKFSKCSILEYHDFLQRGGAC	491
Dd	309	SLAQNGLIGIOWEPSRRPKCDCTESMGCI MEETGVSHSRKFSKCSILEYHDFLQRGGAC	368
QY	492	LENRPKLFEEPEECGNGVYEAGEECOCGFFVEYGLCKCKKCSLSNAGHSDGQCCNNTSC	551
Dd	369	LENRPKLFEEPEECGNGVYEAGEECOCGFFVEYGLCKCKKCSLSNAGHSDGQCCNNTSC	428
QY	552	LFOPRGYECRDVAVNECDITEYCTGDSGQCPRLNHLKQDGYACNANOGRGCVGEKTRDNOG	611
Dd	429	LFOPRGYECRDVAVNECDITEYCTGDSGQCPRLNHLKQDGYACNANOGRGCVGEKTRDNOG	488
QY	612	OYIMKTKAAGSUKPCYEKLNTEGTEKNGCKQKQDRKIQCSKHVFCGFLLCITNLTAAPRI	671
Dd	489	OYIMKTKAAGSUKPCYEKLNTEGTEKNGCKQKQDRKIQCSKHVFCGFLLCITNLTAAPRI	548
QY	672	GOLQGEIIFPTSYHOGRVYIDCSGAVHLDDBTDVGVGEDEGTFPCGSPSMCLDRKCLDIOAL	731
Dd	549	GOLQGEIIFPTSYHOGRVYIDCSGAVHLDDBTDVGVGEDEGTFPCGSPSMCLDRKCLDIOAL	608
QY	732	NMSSCPPLSKGCVGCGHGVCSNEATCICDFTYAGADTCSITRDYRNHLHPKDEGPGK	787
Dd	609	NMSSCPPLSKGCVGCGHGVCSNEATCICDFTYAGADTCSITRDYRNHLHPKDEGPGK	664

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: RESULT3
: US-09-809-617-2
: Sequence 2, Application US/09809617
: Patent No. US20020131778A1
: GENERAL INFORMATION:
: APPLICANT: Sheppard, Paul O.
: APPLICANT: Baidur, Mend
: APPLICANT: Delshet, Theresa A.
: APPLICANT: Bishop, Paul D.
: TITLE OF INVENTION: DISINTEGRIN HOMOLOG
: FILE REFERENCE: 98-29
: CURRENT APPLICATION NUMBER: US/09/809,617
: PRIOR FILING DATE: 2001-03-15
: PRIOR APPLICATION NUMBER: US/09/351,414
: PRIOR FILING DATE: 1999-07-09
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 696
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-809-617-2

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	Query Match	79.5%	Score 3621	DB 10	Length 696
Best Local Similarity	99.7%	Pred. No. 1.3e-237			
Matches 654	Conservative	0	Mismatches 2	Incls 0	Gaps 0
QY	132	LDTARHQKINKVAVHLAQASFOEAFGSKPTLDLILNGLLSSDYVEIHENGKPYQSK	191		



Db 237 LIETANYDKFYR-SLNIRIALVGLVWTHGNMCEVSENPYSTLWSEFLSWRRKLLAOKYH 295  
OY 384 DAVHLISRYTFHYKRSLSYFGVCS--RTRGVVNEGYGLPMAVAOYLSOSLAONIGIOW 441  
Db 296 DNAQLITGMSFHGTITGLAPLMAVCVYOSGVNMDHSENAIGVATMAHEMGNHGMTH 355  
OY 442 EPSRKRKCDCTESWGCIH-EETGVSHSRKFSKSILEYRDLORGACLEFNRP--TK 498  
Db 356 DSAD--CCSASADGCIIMAAATGHPFKVFNCGNRRLDRYLDSGGGMCLSNMPDTRM 412  
OY 499 LFEPTGNGVYVAGEECCGFHVECYGLCC--KKCSLSNGAHGSDGCCNNTSCLFQPR 556  
Db 413 LVGGRGNGYLEDGEECCGEECCNPNCCNASNCTLRPGAECAGHSCCH--QCKLLAP 470  
OY 557 GYECDAVNECDITEYCTGDSGCCPPNLHKODGYACNONGRCYGECKTRNOCQYIWG 616  
Db 471 GTLCREQARQCDLPECTGKSPHCPTNFYOMDGTCEGGQAYCINMCLTYOEOCQOLMG 530  
OY 617 TRAGSDKFCYKLTBEGTEKNGCKD-GDRMIQCSKHDPVCGFLCTNLTRAPRIGOLQ 675  
Db 531 PGARPAJDICEKVNAGDTFGNCGKDMNGEHRKCMRDAKCGKIQQCSSEARP----LE 586  
OY 676 GEIIP--TSFYHOGVYIDCSGAHVYL-----DDDTGVYVEDGTFCGSPSMCLDRKCLQI 728  
Db 587 SNAVIDITTIMNGRQICRGTHYRGPEEGDMLDPLVMTGKCGYNHICFEGOCNRT 646  
OY 729 QALNMSCPLDSKGVCSGHVCSNEATCICDFTWAGTDCSIRDPVRLHPPKDEGPKGP 788  
Db 647 SFEETEGC-----GKCKNGHGVCCNNONCHCLPGMAPFCNTPGHGSII-----DSGPMPP 697  
OY 789 SATNLIIGSAGAILVAIVL 809  
Db 698 ESVGPVVAGVLAIVLVAIVLM 718

## RESULT 6

US-10-125-452-16  
Sequence 16, Application US/10125452  
Patent No. US20020173640A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: ADAM Polynucleotides, Polypeptides, and Antibodies  
FILE REFERENCE: PTO06P2  
CURRENT APPLICATION NUMBER: US/10/125,452  
CURRENT FILING DATE: 2002-04-19  
PRIOR APPLICATION NUMBER: 09/955,504  
PRIOR FILING DATE: 2001-09-19  
PRIOR APPLICATION NUMBER: 09/712,907  
PRIOR FILING DATE: 2000-11-16  
PRIOR APPLICATION NUMBER: PCT/US00/14308  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: 60/178,717  
PRIOR FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: 60/142,930  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: 60/136,388  
PRIOR FILING DATE: 1999-05-27  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 16  
LENGTH: 778  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-125-452-16

## Query Match

22.1% Score 1007.5; DB 9; Length 778;  
Best Local Similarity 31.5%; Pred. No. 31e-60;  
Matches 252; Conservative 111; Mismatches 325; Indels 113; Gaps 29;

OY 38 PARTPCRLVLLPLPLAASRRPANGAAPSAPHNNETAENKLVGLADEDNLTQONS 97  
Db 2 PEGAGAAARCLIAFALQPL--RBR-----AAREPGMTRSEEB----- 37

OY 98 SSNISYSNAMOKEITLPSRLIYIYNODESEPYHVLDTKARRHOQKANKAVHLAQSFOLEA 157  
Db 38 -----SPKQLDHELIIPW-----KTSESIV-----REKHPKLKELVMA 71  
OY 158 FGSKTIDLLIUNGLSSDYVEIHV-ENGKPOYS--KGECHYHGSIRGVKDSKVALST 214  
Db 72 EGRELIDLEKNEDLFAPSYETETHYSSGNQOTTRKLEDCFHGVHIVRELESSLVLTST 131  
OY 215 CNGLHGMFE-DDTIVYMEPELHVDEKSTGRPHILIKTLAQVSKQMK-----NLTMERG 269  
Db 132 CRGIRGLTIVSSNLSTYIEPLP---DSKG---QHLIYR-----SEHLKRPFGCGFEHS 179  
OY 270 D-----QWPELSELQMLKRRRAVNPSSRGIFEEMKYLEIMVINDKTKYKRRSHAHNNF 325  
Db 180 KPTTRDMA-LOFTQOTKKRPRM--KREDLSMKYVELIVADYLEQKKRRQODATKHK 236  
OY 326 AKSVNIVYDSIYKQOLMTRVYLVAVETWTERKQDIDITNPVOMLHESKYRORI--KQHA 383  
Db 237 LIETANYDKFYR-SLNIRIALVGLVWTHGNMCEVSENPYSTLWSEFLSWRRKLLAOKYH 295  
OY 384 DAVHLISRYTFHYKRSLSYFGVCS--RTRGVVNEGYGLPMAVAOYLSOSLAONIGIOW 441  
Db 296 DNAQLITGMSFHGTITGLAPLMAVCVYOSGVNMDHSENAIGVATMAHEMGNHGMTH 355  
OY 442 EPSRKRKCDCTESWGCIH-EETGVSHSRKFSKSILEYRDLORGACLEFNRP--TK 498  
Db 356 DSAD--CCSASADGCIIMAAATGHPFKVFNCGNRRLDRYLDSGGGMCLSNMPDTRM 412  
OY 499 LFEPTGNGVYVAGEECCGFHVECYGLCC--KKCSLSNGAHGSDGCCNNTSCLFQPR 556  
Db 413 LVGGRGNGYLEDGEECCGEECCNPNCCNASNCTLRPGAECAGHSCCH--QCKLLAP 470  
OY 557 GYECDAVNECDITEYCTGDSGCCPPNLHKODGYACNONGRCYGECKTRNOCQYIWG 616  
Db 471 GTLCREQARQCDLPECTGKSPHCPTNFYOMDGTCEGGQAYCINMCLTYOEOCQOLMG 530  
OY 617 TRAGSDKFCYKLTBEGTEKNGCKD-GDRMIQCSKHDPVCGFLCTNLTRAPRIGOLQ 675  
Db 531 PGARPAJDICEKVNAGDTFGNCGKDMNGEHRKCMRDAKCGKIQQCSSEARP----LE 586  
OY 676 GEIIP--TSFYHOGVYIDCSGAHVYL-----DDDTGVYVEDGTFCGSPSMCLDRKCLQI 728  
Db 587 SNAVIDITTIMNGRQICRGTHYRGPEEGDMLDPLVMTGKCGYNHICFEGOCNRT 646  
OY 729 QALNMSCPLDSKGVCSGHVCSNEATCICDFTWAGTDCSIRDPVRLHPPKDEGPKGP 788  
Db 647 SFEETEGC-----GKCKNGHGVCCNNONCHCLPGMAPFCNTPGHGSII-----DSGPMPP 697  
OY 789 SATNLIIGSAGAILVAIVL 809  
Db 698 ESVGPVVAGVLAIVLVAIVLM 718

## RESULT 7

US-09-955-504-16  
Sequence 16, Application US/09955504  
Publication No. US20020182702A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: ADAM Polynucleotides, Polypeptides, and Antibodies  
FILE REFERENCE: PTO06P2  
CURRENT APPLICATION NUMBER: US/09/955,504  
CURRENT FILING DATE: 2001-09-19  
PRIOR APPLICATION NUMBER: 60/234,222  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: 09/712,907  
PRIOR FILING DATE: 2000-11-16  
PRIOR APPLICATION NUMBER: PCT/US00/14308  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: 60/178,717  
PRIOR FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: 60/142,930  
PRIOR FILING DATE: 1999-07-09

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; PRIOR APPLICATION NUMBER: 60/136,388
; PRIOR FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 16
; LENGTH: 778
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-955-504-16

Query Match      22.1% Score 1007.5; DB 9; Length 778;
Best Local Similarity 31.5%; Pred. No. 3.1e-60;
Matches 252; Conservative 111; Mismatches 325; Indels 113; Gaps 29;

OY 38 PARTPCRLVLLPRLAASSPRAMGAAPSPHNMETAENKVLADENNTLOONS 97
DB 2 PGAGAAALCLLAFALQPL---RPR-----AAREPCWTRGSEEG----- 37
OY 98 SSNISTYNNAMOKETLPSRLIYIYNODESPYHVLDTKARHQQKNKAVHLAQAFOIEA 157
DB 38 -----SPKLOHLLIPQW-----KTSESPV-----REKHPKLKELR/MA 71
OY 158 FGSKEFLDLLNGLSSDYVEIHY-ENGKPOYS--KGGEHCYHNSIRGVKDSKVALST 214
DB 72 EGEELLIDLEKNEQLFAPSYTETHHTSSGNPQTTTKRLIEDHCFHGVETELSSVLTST 131
OY 215 CNGLHGMEF-DTFEYVMIPELVELVHDEKSTGRPHIIOKTLAOGYSKOMK-----NLTMERG 269
DB 132 CRGIGLITVSSNLSYVEIPLP---DSKG---QHLYIR-----SEHLKPRPGNGCFEHS 179
OY 270 D-----QMPFLSELQMLKRRRAVNPSPRGIFEEMKYLELMIVNDHKTYKKHRSNAHTNNF 325
DB 180 KPTTRDMA-LOFTQOTKKRRPRM--KREDLNSMKYVELVADYLEFOKNRRDQATKHK 236
OY 326 AKSVNVLVDSTYKEQLNTRVVLAVETWTEKQDIDITTPVOMLHEFSKYRORI--KQHA 383
DB 237 LIEIANYVDKFR-SLNIRIALVGLVMTWTHGNMCEVSENPYSTLMSFLSMRKLKLAOKYH 295
OY 384 DAVHLISRVTFFHYKRSLSYFGVCS--RTRGVGVNEYGLPMAVAOYLSQSLAQNIGTOW 441
DB 296 DNAQLITGMSFHGTTIGLAPLMAKCSYVQSGGVNMDHSENAIGVATMAHEMGNHFGMTI 355
OY 442 EPSSRRPKCDCTESWGGLM-EETGVSHSRKFSKCSILEYRDLQRCGGACLPNRP--TK 498
DB 356 DSAD---CCSASADGGCIMAATGHPFPKVFNGCNRRELDRYLQSGGCMCLSNMPTDM 412
OY 499 LEPTGCGNGYVAGEECDCGFFHVECYGLCC--KKSLSNGAHNSDPCPCNNTSCLEPQR 556
DB 413 LYGGRGCKNGYLEDGEDCEDEECNNPCCNASNCTLRPGAECARHSCCH--QCKLLAP 470
OY 557 GYECRDVAVNECDITTEYCTGDSGOCPPNLIHKODYACNONOGRACYNGECKTRDNOCQYIWG 616
DB 471 GTLCREQARQCDLPREFCTGKSPHCPTNFYQMDGTRPCGGQAYCYNGMCLTYQEOCCQOLWG 530
OY 617 TKAAGSDKFCYEKLNTBETGKNGCKD-GDRMIQCSKHDVFCGFLCTLNLTAPRIGTQLO 675
DB 531 PGARPARDLCEFEKVVNAGDTFGNGCKDMNGEHRKCNMRDAKCGKIQOCSSEARP---LE 586
OY 676 GEIIP--TSFYHOGVAVIDCSGAHYVL-----DDDTVGYVEDGTRPCSPMIMCLDRKCIQI 728
DB 587 SNAVPIIDTTIIMNGROIQCRGTHVYRGPREEGMDLDPGLVMTGTCKGCVNHICFEGGCFRNT 646
OY 729 QALNMSSCPPLDSKGVCSGHGVCSENEATYICIDFTWAGTDCSIRDPVRNLIHPKDEGPKRP 788
DB 647 SEFTEGEC-----GKKCNHGVCHNNONCHCLPGMARPPFCNTPRHGCSI-----DSGPRVPR 697
OY 789 SATNLIISIGAILIYAIVL 809
DB 698 ESVGPRVAGVAILVAILVAVLM 718

RESULT 8
US-10-020-733-4
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; Sequence 4, Application US/10020733
; Patent No. US20020161214A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilgenowski, Nathaniel L.
; APPLICANT: Fiddie, Carl Johan
; TITLE OF INVENTION: NO. US20020161214A1 Human Proteases and Polynucleotides Enco
; FILE REFERENCE: LEX-0263-USA
; CURRENT APPLICATION NUMBER: US/10/020,733
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: US 60/244,939
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 918
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-020-733-4

Query Match      22.1% Score 1007.5; DB 9; Length 918;
Best Local Similarity 31.5%; Pred. No. 3.9e-60;
Matches 252; Conservative 111; Mismatches 325; Indels 113; Gaps 29;

OY 38 PARTPCRLVLLPRLAASSPRAMGAAPSPHNMETAENKVLADENNTLOONS 97
DB 2 PGAGAAALCLLAFALQPL---RPR-----AAREPCWTRGSEEG----- 37
OY 98 SSNISTYNNAMOKETLPSRLIYIYNODESPYHVLDTKARHQQKNKAVHLAQAFOIEA 157
DB 38 -----SPKLOHLLIPQW-----KTSESPV-----REKHPKLKELR/MA 71
OY 158 FGSKEFLDLLNGLSSDYVEIHY-ENGKPOYS--KGGEHCYHNSIRGVKDSKVALST 214
DB 72 EGEELLIDLEKNEQLFAPSYTETHHTSSGNPQTTTKRLIEDHCFHGVETELSSVLTST 131
OY 215 CNGLHGMEF-DTFEYVMIPELVELVHDEKSTGRPHIIOKTLAOGYSKOMK-----NLTMERG 269
DB 132 CRGIGLITVSSNLSYVEIPLP---DSKG---QHLYIR-----SEHLKPRPGNGCFEHS 179
OY 270 D-----QMPFLSELQMLKRRRAVNPSPRGIFEEMKYLELMIVNDHKTYKKHRSNAHTNNF 325
DB 180 KPTTRDMA-LOFTQOTKKRRPRM--KREDLNSMKYVELVADYLEFOKNRRDQATKHK 236
OY 326 AKSVNVLVDSTYKEQLNTRVVLAVETWTEKQDIDITTPVOMLHEFSKYRORI--KQHA 383
DB 237 LIEIANYVDKFR-SLNIRIALVGLVMTWTHGNMCEVSENPYSTLMSFLSMRKLKLAOKYH 295
OY 384 DAVHLISRVTFFHYKRSLSYFGVCS--RTRGVGVNEYGLPMAVAOYLSQSLAQNIGTOW 441
DB 296 DNAQLITGMSFHGTTIGLAPLMAKCSYVQSGGVNMDHSENAIGVATMAHEMGNHFGMTI 355
OY 442 EPSSRRPKCDCTESWGGLM-EETGVSHSRKFSKCSILEYRDLQRCGGACLPNRP--TK 498
DB 356 DSAD---CCSASADGGCIMAATGHPFPKVFNGCNRRELDRYLQSGGCMCLSNMPTDM 412
OY 499 LEPTGCGNGYVAGEECDCGFFHVECYGLCC--KKSLSNGAHNSDPCPCNNTSCLEPQR 556
DB 413 LYGGRGCKNGYLEDGEDCEDEECNNPCCNASNCTLRPGAECARHSCCH--QCKLLAP 470
OY 557 GYECRDVAVNECDITTEYCTGDSGOCPPNLIHKODYACNONOGRACYNGECKTRDNOCQYIWG 616
DB 471 GTLCREQARQCDLPREFCTGKSPHCPTNFYQMDGTRPCGGQAYCYNGMCLTYQEOCCQOLWG 530
OY 617 TKAAGSDKFCYEKLNTBETGKNGCKD-GDRMIQCSKHDVFCGFLCTLNLTAPRIGTQLO 675
DB 531 PGARPARDLCEFEKVVNAGDTFGNGCKDMNGEHRKCNMRDAKCGKIQOCSSEARP---LE 586
OY 676 GEIIP--TSFYHOGVAVIDCSGAHYVL-----DDDTVGYVEDGTRPCSPMIMCLDRKCIQI 728
DB 587 SNAVPIIDTTIIMNGROIQCRGTHVYRGPREEGMDLDPGLVMTGTCKGCVNHICFEGGCFRNT 646
OY 729 QALNMSSCPPLDSKGVCSGHGVCSENEATYICIDFTWAGTDCSIRDPVRNLIHPKDEGPKRP 788
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Db 647 SFFTEGCG-----GKCKGHCVCNNNONCHCLPQMAAPFCNTPGHGSI-----DSGEMPP 697

Qy 789 SATNLIIGSINGAILVAIVL 809

Db 698 ESVGPPVAGVAILVAILVAILM 718

RESULT 9

US-10-125-470-9

Sequence 9, Application US/10125470

Patent No. US20020165377A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: ADAM Polynucleotides, Polypeptides, and Antibodies

FILE REFERENCE: PT006P1

CURRENT APPLICATION NUMBER: US/10/125,470

PRIOR FILING DATE: 2002-04-19

PRIOR APPLICATION NUMBER: US/09/712,907A

PRIOR FILING DATE: 2001-03-07

PRIOR APPLICATION NUMBER: 60/136,388

PRIOR FILING DATE: 1999-05-27

PRIOR APPLICATION NUMBER: 60/142,930

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: 60/178,717

PRIOR FILING DATE: 2000-01-28

NUMBER OF SEQ ID NOS: 24

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 9

LENGTH: 918

TYPE: PRT

ORGANISM: Homo sapiens

US-10-125-470-9

Query Match 22.1%; Score 1007.5; DB 9; Length 918;

Best Local Similarity 31.5%; Pred. No. 3.9e-60;

Matches 252; Conservative 111; Mismatches 325; Indels 113; Gaps 29;

Qy 38 PARPPCRLVLLVLLPLLAASSRPRANGAAPSAPHNNETEKMLGVLADENLTLOONS 97

Db 2 PGAGAAALCLLAFALQPL-----RPR-----AAREPGWTRGSEEG----- 37

Qy 98 SSNISYSNAMOKEITLPSRLIYIYNODESPYHVLDTKAHQOKHNKAVHLAASFOIEA 157

Db 38 -----SPKLQHELIIPQW-----KTSSEPV-----REKHPKLAELRVMA 71

Qy 158 FGSKFILDLLNGLSSDYVEIHY-ENGKPOYS--KGGEHCYHGSIRGVKDSKVALST 214

Db 72 EGRELIDLEKNEQLFAPSYTEHTYSSGNPQTTTRKLEDHCFYHGTVRETELSSVTLST 131

Qy 215 CNGLHGME-DDTFYVMTPELVLHDEKSTGRPHIIOKTLAOGYSKOMK-----NLIMERG 269

Db 132 CRGIGLTLVSSNSLSYIEPLP---DSKG---OHLIYR-----SEHLRPPGNCGEFHS 179

Qy 270 D-----QMPFLSELQWLKRRRAVNPSSRGIFEEMKYLELMIVNDHKTYKKRRSSHAHTNPF 325

Db 180 KPTTQDMA-LOFTQOTKKRRRM--KREDLNMKYVELVLADYLEFOKNRRDQATKHX 236

Qy 336 AKSVNVLVDISYKEQNLTRVVLAVETWTEKQIDITTPVOMLHEFSKYRQRI--KQHA 383

Db 237 LLEIANVYDKFYR-SLIRIALVGLVEMTHGNMCSEVSEPTLMSFLSWRRRLAOKXH 295

Qy 384 DAVHLISRTVEHYKSSLSYFGVCS--RTRGVGYVEYGLPMAVAVLQVLSLQNTGIOM 441

Db 236 DNAQILTGSPFTTIGLAPLMAKMSVYOSGGVNMDSHENSALGVAATMAHEMHNMGTH 355

Qy 442 EPPSKRPKDCETESWGGCIM-EETGVSHSRKSKSCSILEYRDLQROGACLPNRP--TK 498

Db 356 DSAD---CCSASADGCGCIMAATGHPKPVFNGCRBELDRYLQSGGWCJLSNMPDTRM 412

Qy 499 LPEPTECGNGYVAGECCGCGFVEVEYGLCC--KKCSLSNGAMCSGPGCCNNTSCLEFQR 556

Db 413 LVGGRGCGNGYLEDGEDCCGEEBECNPNCCNASNCTLRPGACAGSGSCH--QCKLAP 470

Qy 557 GECRDVAVNECDITTEYCTGDSGCPENLHKODGYACANONQRCYNGECKTRDNOCQYIMG 616

Db 471 GTLCREQARQCDLDEFCFGKSPHCPTNTYOMDGTPEBGGAYCYNGMKLTYQEOCQOLMG 530

Qy 617 TRAGSDKCEYKELNTEGTEKNGCKGD-GDRWIOCSKHDFCGELCTNLTRAPRIGLO 675

Db 531 PGARPAPDLCEFEKVAVADTFEGNCGKDMNGEHRKCMMDKACGKIQCOSSEARP-----LE 586

Qy 676 GEIIP--ISFYHOGAVIDCSGAHYVL-----DDDTVGVEDEGTPCGSPMCLDRKCLQI 728

Db 587 SNAVEIDTITLMNGHQIQCRGTHVTRGPEEBSDMLPBLVMTGTGCGTNHICFEQCCANT 646

Qy 729 QALNMSCPDLSKGVCSGHGVCSEATCICDFTWAGTDCSIRDPVRNLHPKDEGPRGP 788

Db 647 SFFTEGCG-----GKCKGHCVCNNNONCHCLPQMAAPFCNTPGHGSI-----DSGEMPP 697

Qy 789 SATNLIIGSINGAILVAIVL 809

Db 698 ESVGPPVAGVAILVAILVAILM 718

RESULT 10

US-10-125-452-9

Sequence 9, Application US/10125452

Patent No. US20020173640A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: ADAM Polynucleotides, Polypeptides, and Antibodies

FILE REFERENCE: PT006P2

CURRENT APPLICATION NUMBER: US/10/125,452

PRIOR FILING DATE: 2002-04-19

PRIOR APPLICATION NUMBER: 09/955,504

PRIOR FILING DATE: 2001-09-19

PRIOR APPLICATION NUMBER: 09/712,907

PRIOR FILING DATE: 2000-11-16

PRIOR APPLICATION NUMBER: PCT/US00/14308

PRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: 60/178,717

PRIOR FILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: 60/142,930

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: 60/136,388

PRIOR FILING DATE: 1999-05-27

NUMBER OF SEQ ID NOS: 38

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 9

LENGTH: 918

TYPE: PRT

ORGANISM: Homo sapiens

US-10-125-452-9

Query Match 22.1%; Score 1007.5; DB 9; Length 918;

Best Local Similarity 31.5%; Pred. No. 3.9e-60;

Matches 252; Conservative 111; Mismatches 325; Indels 113; Gaps 29;

Qy 38 PARPPCRLVLLVLLPLLAASSRPRANGAAPSAPHNNETAEKNLGLVADENLTLOONS 97

Db 2 PGAGAAARCLLAFALQPL-----RPR-----AAREPGWTRGSEEG----- 37

Qy 98 SSNISYSNAMOKEITLPSRLIYIYNODESPYHVLDTKAHQOKHNKAVHLAASFOIEA 157

Db 38 -----SPKLQHELIIPQW-----KTSSEPV-----REKHPKLAELRVMA 71

Qy 158 FGSKFILDLLNGLSSDYVEIHY-ENGKPOYS--KGGEHCYHGSIRGVKDSKVALST 214

Db 72 EGRELIDLEKNEQLFAPSYTEHTYSSGNPQTTTRKLEDHCFYHGTVRETELSSVTLST 131

Qy 215 CNGLHGME-DDTFYVMTPELVLHDEKSTGRPHIIOKTLAOGYSKOMK-----NLIMERG 269

Db 132 CRGIGLTLVSSNSLSYIEPLP---DSKG---OHLIYR-----SEHLRPPGNCGEFHS 179

Qy 270 D-----QMPFLSELQWLKRRRAVNPSSRGIFEEMKYLELMIVNDHKTYKKRRSSHAHTNPF 325



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      180 KPTTRDMA-LOFTOOTKKRRPRM--KREDLNSMKYVELYLAVADYLEFOKNRRDODATYHK 236
      326 AKSVNLVDSIYKQLNTRVLVAVETWTEKDOIITFNPMQMLHEFSKYRORI--KQHA 383
      237 LLEIANYVDKPYR-SLIRIALVGLVWTHGNMCEVSENPSTLWSPSLMRKLLAQYH 295
      384 DAVHLISRYTFHYKRSSLSYFGVCS--RTRGVNEYGLPMAVAQVLSOSLAQNLGIOW 441
      296 DNQOLITGMSFHGTITGLAPLMAVCYQSGVNMDSHSENAIGVAATMAHEMGNHFGMTH 355
      442 EPSSRRKPKDCSTESWGCIM-EETGVSHSRKFSKCSILEYRDLORGGACLEFNR--TK 498
      356 DSAD--CCSASADGGCIMAATAAGHPKPYFNGCNRELDRLYLQSGGCMCLSNMPTRM 412
      499 LPEPTGCGVYEGAGECCGFHECYGLCC--KCSLSNGAHCSDDGCSNNISCLFEPFR 556
      413 LYGRRCNGVLEDEGECCDCEEECCNPPCCNASNCTLRPGAECAGHSCCH--QCKLLAP 470
      557 GYECRDVAVNECDITTEYCTGDSGOCPPNLHKODGYACNONOGRCYNGECKTRDNOCQYIWG 616
      471 GTLCRQARQCDLPEFCTGKSPHCPTNPFYQMDGTPCEGGAUYCYNGMCLTYOEQOQOLWG 530
      617 TKAAGSKFCEYKANTGTEKNGCKD-GDRWIOCSKHDFVCGFLCTNLTRAPRIGLO 675
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      676 GEIIP--TSFYHOGRVIDSGAHVVL-----DDTDVGYVEDTGPCGSPMCLDRKLOI 728
      587 SNAVPIDITTIIMNGROIQCRGTHYVRGPEEGMDLPGLVMTGTCGYNHICFEQOCNRT 546
      729 QALNMSSCPIDSKGVCSGHVCSENEATCICDFTWAGTDCSIRDPVRNLHPKDEGPKP 788
      647 SFETEGC-----GKCKNGHGVCCNNONCHCLPGMAPRPFCTNPGHGSI-----DSGMP 597
      789 SATNLIIGSIAGALVLAIVL 809
      698 ESVGPAVAGVLAIVLAVLM 718

      RESULT 11
      US-09-955-504-9
      ; Sequence 9, Application US/09955504
      ; Publication No. US20020182702A1
      ; GENERAL INFORMATION:
      ; APPLICANT: Ruben et al.
      ; TITLE OF INVENTION: ADAM Polynucleotides, Polypeptides, and Antibodies
      ; FILE REFERENCE: PTO06P2
      ; CURRENT APPLICATION NUMBER: US/09/955, 504
      ; CURRENT FILING DATE: 2001-09-19
      ; PRIOR APPLICATION NUMBER: 60/234, 222
      ; PRIOR FILING DATE: 2000-09-21
      ; PRIOR APPLICATION NUMBER: 09/712, 907
      ; PRIOR FILING DATE: 2000-11-16
      ; PRIOR APPLICATION NUMBER: PCT/US00/14308
      ; PRIOR FILING DATE: 2000-05-25
      ; PRIOR APPLICATION NUMBER: 60/178, 717
      ; PRIOR FILING DATE: 2000-01-28
      ; PRIOR APPLICATION NUMBER: 60/142, 930
      ; PRIOR FILING DATE: 1999-07-09
      ; PRIOR APPLICATION NUMBER: 60/136, 388
      ; PRIOR FILING DATE: 1999-05-27
      ; NUMBER OF SEQ ID NOS: 38
      ; SOFTWARE: PatentIn Ver. 2.0
      ; SEQ ID NO 9
      ; LENGTH: 918
      ; TYPE: PRT
      ; ORGANISM: Homo sapiens
      ; US-09-955-504-9

      Query Match 22.1%, Score 1007.5; DB 9; Length 918;
      Best Local Similarity 31.5%, Pred. No. 3.9e-60;
      Matches 252; Conservative 111; Mismatches 325; Indels 113; Gaps 29;
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      38 PARTPCRLILLVLLPLPLAASSPRAMGAAPASAPHHNETAKNGLVLADEDNITLOONS 97
      2 PGAGAACRLCLLAFNLPL-----RPR-----AAREGWTGRGSEGE-----37
      98 SSNISYSNMQKEITPLPSRLIYYINODESPYHVLDTKARHQQKHNKAVHQAOSFOIEA 157
      38 -----SPKLQHELLIPQW-----KTSSEPV-----REKHPRLKAELVMA 71
      158 FCSKFLIDLILNGLLSSIVYEIHY-ENGRPOVS--KGEHCYHHSIRKVRKSKVALST 214
      72 EGRELLIDLEKNEQLFAPSYLETTHYSSGNPQTTTRKLEDHCYHGTVRETELSSVTLST 131
      215 CUGLHMFED-DTFYMIPLLELVHEKDECTGRPHIIOKTLAOGYSKOMK-----NLTMERG 269
      132 CGIGIGLIVSSNLSVIEPLP---DSKG---OHLYR-----SEHLKRPNGCFEHS 179
      180 KPTTRDMA-LOFTOOTKKRRPRM--KREDLNSMKYVELYLAVADYLEFOKNRRDODATYHK 236
      326 AKSVNLVDSIYKQLNTRVLVAVETWTEKDOIITFNPMQMLHEFSKYRORI--KQHA 383
      237 LLEIANYVDKPYR-SLIRIALVGLVWTHGNMCEVSENPSTLWSPSLMRKLLAQYH 295
      384 DAVHLISRYTFHYKRSSLSYFGVCS--RTRGVNEYGLPMAVAQVLSOSLAQNLGIOW 441
      296 DNQOLITGMSFHGTITGLAPLMAVCYQSGVNMDSHSENAIGVAATMAHEMGNHFGMTH 355
      442 EPSSRRKPKDCSTESWGCIM-EETGVSHSRKFSKCSILEYRDLORGGACLEFNR--TK 498
      356 DSAD--CCSASADGGCIMAATAAGHPKPYFNGCNRELDRLYLQSGGCMCLSNMPTRM 412
      499 LPEPTGCGVYEGAGECCGFHECYGLCC--KCSLSNGAHCSDDGCSNNISCLFEPFR 556
      413 LYGRRCNGVLEDEGECCDCEEECCNPPCCNASNCTLRPGAECAGHSCCH--QCKLLAP 470
      557 GYECRDVAVNECDITTEYCTGDSGOCPPNLHKODGYACNONOGRCYNGECKTRDNOCQYIWG 616
      471 GTLCRQARQCDLPEFCTGKSPHCPTNPFYQMDGTPCEGGAUYCYNGMCLTYOEQOQOLWG 530
      617 TKAAGSKFCEYKANTGTEKNGCKD-GDRWIOCSKHDFVCGFLCTNLTRAPRIGLO 675
      531 PGARPADLCEFEKYNVAGDTFGNCGKDMNGEHRKCNMRDAKCGKIOCCSSEARP---LE 586
      676 GEIIP--TSFYHOGRVIDSGAHVVL-----DDTDVGYVEDTGPCGSPMCLDRKLOI 728
      587 SNAVPIDITTIIMNGROIQCRGTHYVRGPEEGMDLPGLVMTGTCGYNHICFEQOCNRT 546
      729 QALNMSSCPIDSKGVCSGHVCSENEATCICDFTWAGTDCSIRDPVRNLHPKDEGPKP 788
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      ; Patent No. US20020161214A1
      ; GENERAL INFORMATION:
      ; APPLICANT: Walke, D. Wade
      ; APPLICANT: Wilgenowski, Nathaniel L.
      ; APPLICANT: Fiddie, Carl Johan
      ; TITLE OF INVENTION: NO. US20020161214A1 Human Proteases and Polynucleotides Enco
      ; FILE REFERENCE: LEX-0263-USA
      ; CURRENT APPLICATION NUMBER: US/10/020, 733
      ; CURRENT FILING DATE: 2001-10-30
      ; PRIOR APPLICATION NUMBER: US 60/244, 939
      ; PRIOR FILING DATE: 2000-11-01
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; SOFTWARE: FastSeq for Windows Version 4.0

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; LENGTH: 926

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US-10-020-733-2

Query Match 22.18; Score 1007.5; DB 9; Length 926;

Best Local Similarity 31.5%; Pred. No. 3,9e-60; Indels 113; Gaps 29;

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus.p2n model

Run on: June 1, 2003, 18:35:01 ; Search time 4542 seconds  
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QY 821 LysArgArgPheAspProThrGlnGlnGlyProIle 832  
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RESULT 2  
US-10-202-675-2  
; Sequence 2, Application US/10202675  
; GENERAL INFORMATION:  
; APPLICANT: Cerrectil, Douglas P.  
; TITLE OF INVENTION: SVP#3-13 AND SVP#3-17 DNA AND POLYPEPTIDES  
; FILE REFERENCE: 03260, 0051-00304  
; CURRENT APPLICATION NUMBER: US/10/202,675  
; CURRENT FILING DATE: 2002-07-23  
; PRIOR APPLICATION NUMBER: US/09/634,252  
; PRIOR FILING DATE: 2000-08-07  
; PRIOR APPLICATION NUMBER: 60/074,310  
; PRIOR FILING DATE: 1998-02-11  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 2499  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-202-675-2  
Alignment Scores:  
Pred. No.: 3,44e-302 Length: 2499  
Score: 4553.00 Matches: 832  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
DB: 42  
US-09-634-252A-4 (1-832) x US-10-202-675-2 (1-2499)  
QY 1 MetLysProProGlySerSerSerArgGlnProProLeuAlaGlyCysSerLeuAlaGly 20  
Db 1 ATGAAAGCCGCGCGGACAGCTCGCGAGCCGCCGCGGCGCTGCAGCTTGCCTGCGCGC 60  
QY 21 AlsSerCysGlyProGlnArgGlyProAlaGlySerValProAlaSerAlaProAlaArg 40  
Db 61 GCTTCTGCGGCGCGGACAGCGGCGCGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCG 120  
QY 41 ThrProCysArgLeuLeuValLeuLeuLeuLeuLeuProProLeuAlaAlaSerSer 60  
Db 121 ACGCGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
QY 61 ArgProArgAlaTrpGlyAlaAlaAlaProSerAlaProHisTrpAsnGluThrAlaGlu 80  
Db 181 CGGCGCGCGCGCGCGCGCGCTGCTGCGCGCGCGCGCGCTGCGCGCGCGCGCGCGCG 240  
QY 81 LysAsnLeuGlyValIleAlaAspGlyAspAsnThrLeuGlnGlnAsnSerSerSerAsn 100  
Db 241 AAAAATTTGGGAGTCTGCGCAGATGAAGACATATTCATTCAGACGAATAGCAGCAGTAT 300  
QY 101 IleSerTyrSerAsnAlaMetGlnLysGluIleThrLeuProSerArgLeuIleTyrTyr 120

|||||  
Db ATCAGTTACACCAATGCATATGCAGAAAGAAATCAACACCTTCACACTATATATAC 360  
OY ILeasnGlnaspSerGlnSerProThyrHisValLeuAspThrLysAlaArgHisGln 140  
OY 121 ILeasnGlnaspSerGlnSerProThyrHisValLeuAspThrLysAlaArgHisGln 140  
Db 361 ATCAACCAAGACTCGAAGAGCCCTTATCACGTTCTTGACACAAAGGACAAACACAGCA 420  
OY 141 LysHisAsnLysAlaValHisLeuAlaGlnAlaSerPheGlnIleGluAlaPheGlySer 160  
Db 421 AAACATATATAGGCTGCTCATCTGGCCACAGCAACCTTCAGATTGAAGCCCTTCGCTCC 480  
OY 161 LysPheIleLeuAspLeuIleLeuAsnAsnGlyLeuLeuSerSerAspThrAlaGluIle 180  
Db 481 AAATTCATCTTGACCTCATCTGACACATGGTTGTTGTTCTTGATTAATGCGAGATT 540  
OY 181 HisTyrGlnAsnGlyLysProGlnTyrSerLysGlyGluHisCysTyrTyrHisGly 200  
Db 541 CACTACGAAATGGGAAACACACACTACTCTAGGGTGGAGACACTGTTACTACACATGGA 600  
OY 201 SerIleArgGlyValLysAspSerLysValAlaLeuSerThrCysAsnGlyLeuHisGly 220  
Db 601 AGCATCAGAGGCGCTCAAGACTCCAAAGGTGGCTGTCAACTGCACATGAGACTTTCATGCG 660  
OY 221 MetPheGluAspAspThrPheValTyrMetIleGluProLeuGluLeuValHisAspGlu 240  
Db 661 ATGTTGAAGATGATACCTTCGTGATATGATAGACCCACTAGAGCTGGTTCATGATGAG 720  
OY 241 LysSerThrGlyArgProHisIleIleGlnLysThrLeuAlaGlyGlnTyrSerLysGln 260  
Db 721 AAACACACAGCTGCACACCATATATCCAGAAACCTTGGCAGACAGATTCATGACAA 780  
OY 261 MetLysAsnLeuThrMetGluArgGlyAspGlnTyrProPheLeuSerGluLeuGlnTyr 280  
Db 781 ATGAAGAATCTCATATGAGAAAGAGGTGACAGTGGCCCTTCTCTCAATTAACAGTGG 840  
OY 281 LeuLysArgArgLysArgAlaValAsnProSerArgGlyIlePheGluGluMetLysTyr 300  
Db 841 TTGAAAAGAGAGAGAGAGAGAGTGAATCCATCAGCTGATATATTTGAAGAAATGAATAT 900  
OY 301 LeuGluLeuMetIleValAsnAspHisLysThrTyrLysLysHisArgSerSerHisAla 320  
Db 901 TTGGAACCTATATGATTGATATGATCAAAACGTTAAGACATGACGCTCTCTCATGCA 960  
OY 321 HisThrAsnAsnPheAlaLysSerValLysAsnLeuValAspSerIleTyrLysGluGln 340  
Db 961 CATACCAACACCTTGCAGAGTCCGTGGTCAACCTTGTGATTCATTTACAGAGAGCAG 1020  
OY 341 LeuAsnThrArgValValLeuValAlaValGluThrTyrThrGluLysAspGlnIleAsp 360  
Db 1021 CTCACACACAGGGTGTCTCGTGGTGTGAGACACCTGGACCTGAGAAAGATCAGATTGAC 1080  
OY 361 IleThrThrAsnProValGlnMetLeuHisGluPheSerLysTyrArgGlnArgIleLys 380  
Db 1081 ATCACCACCAACCTTGCAGATGCTCATGAGTTCACAAATACCGGCGACGCATTAAG 1140  
OY 381 GlnHisAlaAspAlaValHisLeuIleSerArgValThrPheHisTyrLysArgSerSer 400  
Db 1141 CAGCAGCTGATGCTGCACTCATCTCGGGGTGATTCATCTAATAAGAGAGACAGT 1200  
OY 401 LeuSerTyrPheGlyGlyValCysSerArgThrArgGlyValGlyAlaAsnGluTyrGly 420  
Db 1201 CTCAGTTACTTTCGAGGTGTCTCTTCGCCACAAGAGAGTGTGGTGTGATGATGATGAT 1260  
OY 421 LeuProMetAlaValAlaGlnValLeuSerGlnSerLeuAlaGlnAsnLeuGlyIleGln 440  
Db 1261 CTTCACATGCGCATGCGCACAGATATATCCACAGAGCTTGCCTCAAAAACCTTGGAAATCAA 1320  
OY 441 TrpGluProSerSerArgLysProLysCysAspCysThrGlnSerTyrGlyGlyCysIle 460  
Db 1321 TGGGAACCTTCTAGCGAAGAAAGCCAAATGATGATCGACAAATCTTGGGTGGCTGATC 1380  
OY 461 MetGluGluThrGlyValSerHisSerArgLysPheSerLysCysSerIleLeuGluTyr 480  
|||||

Db 1381 ATGAGAGAAACAGGGGTGTCCCATTCGCAAAATTTTCAAAATTCGACGATTTGGAGTAT 1440  
OY 481 ArgAspPheLeuGlnArgGlyGlyAlaCysLeuPheAsnArgProThrLysLeuPhe 500  
Db 1441 AGAGACTTTTTCACAGAGAGAGAGGTGAGGCTCCCTTTCACAGAGCCAAACCAAGCTATTT 1500  
OY 501 GluProThrGluCysGlyValAsnGlyTyrValIleAlaGlyGlyGlyCysAspCysGlyPhe 520  
Db 1501 GAGCCACAGGAAATGTGGAAATGATACGTGGAAGCTGGGAGAGAGTGTGATGTTGGTTT 1560  
OY 521 HisValGluCysTyrGlyLeuCysCysLysLysCysSerLeuSerAsnGlyAlaHisCys 540  
Db 1561 CATGTGAATGCTATAGCATATATGCTGTAGAAATGTTCCCTCCCAACGGGCTCATCTCC 1620  
OY 541 SerAspGlyProCysCysAsnAsnThrSerCysLeuPheGluProArgLysTyrGlyCys 560  
Db 1621 AGCGAGGGCCCTGCGTGAACATACCTCATGCTTTTTCAGCCACAGAGGATGATATCC 1680  
OY 561 ArgAspAlaValAsnGluCysAspIleThrGluTyrCysThrGlyAspSerGlyGlnCys 580  
Db 1681 CGGAGTGTGTGACAGAGTGTATATTACTGAATATTGTACTGAGACTCTGGTCACTGC 1740  
OY 581 ProProAsnLeuHisLysGlnAspGlyTyrAlaCysAsnGlnAsnGlnGlyArgCysTyr 600  
Db 1741 CCACCAATCTTCATATAGCAAGACGATATGATGCAATCAAAATCAGGCGCTGCTAC 1800  
OY 601 AsnGlyGluCysLysThrArgAspAsnGlnCysGlnTyrIleThrProLysThrLysAlaIle 620  
Db 1801 AATGGCGAGTGCAGACACAGAGCAACAGTGCATCATCTCGGGCAACAAAGGCTGCA 1860  
OY 621 GlySerAspLysPheCysTyrGlyLysLeuAsnThrGluGlyThrLysGlyAsnCys 640  
Db 1861 GGGTCTGACAGTCTTCATATGAAAAGCTGAATACAGAAAGCGCATGAGAAAGAACTGC 1920  
OY 641 GlyLysAspGlyAspArgTrpIleGlnCysSerLysHisAspValPheCysGlyPheLeu 660  
Db 1921 GGGAGAGATGACAGCGGTGATTCAGTGCAGCAACATGATGCTGTCTGTGATTCCTTA 1980  
OY 661 LeuCysThrAsnLeuThrArgAlaProArgIleGluGluLeuGlnGlyIleIlePro 680  
Db 1981 CTCTGTACCATCTTACTCGAGCTCCACGTATTTGGTCACTTGAAGGTGAGATCATTTCCA 2040  
OY 681 ThrSerPheTyrHisGlnGlyArgValIleAspCysSerGlyAlaHisValValLeuAsp 700  
Db 2041 ACTTCCCTTACCATCAAGCGCGGTGATTGACTGACGTGCGCATGTATGATTTAGAT 2100  
OY 701 AspAspThrAspValGlyTyrValGluAspGlyThrProCysGlyProSerMetMetCys 720  
Db 2101 GATGATACGGATGTGGCTATGTAGAAGATGAAGCCGATGTGGCCGTATGATGATGT 2160  
OY 721 LeuAspArgLysCysLeuGlnIleGlnAlaLeuAsnMetSerSerCysProLeuAspSer 740  
Db 2161 TTAGATCGGAGTGTCCCTCAAAATTCAGCCCTAAATTTGAGACAGCTCCACATGATTC 2220  
OY 741 LysGlyLysValCysSerGlyHisGlyValCysSerAsnGluAlaThrCysIleCysAsp 760  
Db 2221 AAGGTTAAAGTGTGTTCGGGCCAATGGGCTGTAGTATGAAGCCACTGCATTTGTAT 2280  
OY 761 PheThrTrpAlaGlyThrAspCysSerIleArgAspProValAlaArgAsnLeuHisProPro 780  
Db 2281 TTACACTGGGCGAGGACAGATTCAGATATCCCGGATCCAGTTAGGAACCTTCACCCCCC 2340  
OY 781 LysAspGluGlyProLysGlyProSerAlaThrAsnLeuIleIleGlySerIleAlaGly 800  
Db 2341 AAGGATTAAGACCCCAAGGGTCTAGTGCCACCAATCTCATAAATAGGCTCATGCGTGGT 2400  
OY 801 AlaIleLeuValAlaAlaIleValIleLeuGlyGlyThrGlyTyrGlyPheLysAsnValLys 820  
Db 2401 GCCATCCCGTGAAGCATATCTCTTGGGGGACAGGCTGGGATTTAAAAATGTCAG 2460  
OY 821 LysArgArgPheAspProThrGlnGlnGlyProIle 832  
Db 2461 AAGAGAAGGTTGATCTACTACGACAAAGGCCCATC 2496  
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Db 2637 AGCGAGGGCCCTGCTGTAACAAATCCTCATCTCTTTTCAAGCCAGAGCGTATGATGTC 2696  
QY ArgAspAlaValAsnGlyCysAspIleThrGluTyrCysThrGlyAspSerGlyIncys 580  
Db 2637 CGGGATGCTGTGACAGAGTGTGATTTACTGATATTTGACTGAGAGACTCTGTGATGTC 2756  
QY ProProAsnLeuHisLysGlnAspGlyTyrAlaCysAsnGlnAsnGlnGlyAragCysTyr 600  
Db 2757 CCACCAATCTTCAATACCAAGACGATATGATCATCAAAATCAGAGCGCTCTAC 2816  
QY AsnGlyGlyCysLysThrArgAspAsnGlnGlyTyrIleThrGlyThrLysAlaAla 620  
Db 2817 AATGGCGAGTGACAGACAGACAGACAGAGTGTGATGATCTGGGGAACAAAGCTGCA 2876  
QY GlySerAspLysPheCysTyrGluLysLeuAsnThrGluGlyThrGluLysGlyAsnCys 640  
Db 2877 GGGCTGACAAATGCTGCTATGAAAGCTGATACAGAAAGCAGACAGAGGAAAGCTGC 2936  
QY GlyLysAspGlyAspArgTrpIleGlnCysSerLysHisAspValPheCysGlyPheLeu 660  
Db 2937 GGGAGAGATGAGACCGGTGATTCAGTCCAGCAACAGATGTCTTGTGTGATTTCTTA 2996  
QY LeuCysThrAsnLeuThrArgAlaProArgIleGlyGlnLeuGlnGlyLysIleIlePro 680  
Db 2997 CTCTGTACCAATCTTACTGAGACTCCAGCTATTGCTCAACTTCAGAGTGAGATTCACA 3056  
QY ThrSerPheTyrHisGlnGlyArgValIleAspCysSerGlyAlaHisValIleAsp 700  
Db 3057 ACTCTCTCTACCAATCAAGCGCGGTGATTCAGTCCAGTGTGCTCCATGATTTAGAT 3116  
QY AspAspThrAspValGlyTyrValGluAspGlyThrProCysGlyProSerMetCys 720  
Db 3117 GATGATACGAGATGGGCTATGTAGAAATGAGAACCCAGTGGCCGCTATGATGTGT 3176  
QY LeuAspArgLysCysLeuGlnIleGlnAlaLeuAsnMetSerSerCysProLeuAspSer 740  
Db 3177 TTAGATCGGAAGTGGCTACAAATTCAGGCCCTAATATGAGCAGTGTCCATCGATTC 3236  
QY LysGlyLysValCysSerGlyHisGlyValCysSerAsnGluAlaThrCysIleCysAsp 760  
Db 3237 AAGGGTAAAGTCTGTGTTGGGGCCATGGGCTGTGTAGTAATGAAAGCCCTGCAATTTGTGAT 3296  
QY PheThrTrpAlaGlyThrAspCysSerIleArgAspProValArgAsnLeuHisProPro 780  
Db 3297 TTCACCTGGGACAGGACAGATTCAGTATCCGGGATTCAGTATGGAACCTTCACCCCCC 3356  
QY LysAspGluGlyProLysGlyProSerAlaThrAsnLeuIleIleGlySerIleAlaGly 800  
Db 3357 AAGATGAAGAGACCCAGAGGCTCTAGTGCACCAATCTCATATAGGCTTCATCGCTGCT 3416  
QY AlaIleLeuValAlaAlaIleValIleGlyGlyThrGlyTrpGlyPheLysAsnValLys 820  
Db 3417 GCCATCTGCTGATACACTATGTCTTGGGGGACAGGCTGGGGATTTTAAATATGTCAG 3476  
QY LysArgArgPheAspProThrGlnGlnGlyProIle 832  
Db 3477 AAGAGAAGCTGATCTCTACTACGAAAGGCCCATC 3512

RESULT 4  
US-09-976-594-61  
; Sequence 61, Application US/09976594  
; GENERAL INFORMATION:  
; APPLICANT: Furness, Michael  
; APPLICANT: Buchinder, Jenny  
; FILE REFERENCE: PA-0041 US  
; CURRENT APPLICATION NUMBER: US/09/976,594  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 60/240,409  
; PRIOR FILING DATE: 2000-10-12  
; NUMBER OF SEQ ID NOS: 1143  
; SOFTWARE: PERL Program  
; SEQ ID NO 61

LENGTH: 6400  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; OTHER INFORMATION: Incyte ID No: 037502.4  
US-09-976-594-61  
Alignment Scores:  
Pred. No.: 1,09e-301 Length: 6400  
Score: 4553.00 Matches: 832  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
US-09-634-252a-4 (1-832) x US-09-976-594-61 (1-6400)  
QY 1 MetLysProProGlySerSerSerArgGlnProProLeuAlaGlyCysSerLeuAlaGly 20  
Db 224 ATGAGAGCCGCGGACAGAGCTCGCGGACGCGCCCTGCGGCTGACCTGCGCGG 283  
QY 21 AlaSerCysGlyProGlnArgGlyProAlaGlySerValProAlaSerAlaProAlaArg 40  
Db 284 GCTTCTGCGGCGCCCAAGCGGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 343  
QY 41 ThrProProCysArgLeuLeuValIleLeuLeuLeuProProLeuAlaIleSer 60  
Db 344 AGCCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 403  
QY 61 ArgProArgAlaTrpLysAlaAlaAlaProSerAlaProHisTrpAsnGlnThrAlaGln 80  
Db 404 CGGCGCGCGCGCGCGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 463  
QY 81 LysAsnLeuGlyValLeuAlaAspGluAspAsnThrLeuGlnGlnAsnSerSerSerAsn 100  
Db 464 AAAAATTTGGAGATCTCTGCGCAGATGAAAGCAATATGCAACAGATGACAGCACTAAT 523  
QY 101 IleSerTyrSerAsnIleMetGlnLysGlnIleThrLeuProSerArgLeuIleTyr 120  
Db 524 ATGAGTTACGCAATCAATGAGAAAGAAATACACTGCTTCAAGACTCATATATTAC 583  
QY 121 IleAsnGlnAspSerGluSerProTyrHisValIleAspThrLysAlaArgHisGln 140  
Db 584 ATCAACCAAGCTCGGAAGCCCTTATCAAGTCTTGACACAAAGCAAGACACAGCAA 643  
QY 141 LysHisAsnLysAlaValHisLeuAlaGlnAlaSerPheGlnIleGluAlaPheGlySer 160  
Db 644 AAACATATATAGGCTGCTGCTGCGCCAGCAAGCTTCCAGATTGAAGCCTTCGCGCTCC 703  
QY 161 LysPheIleLeuAspLeuIleLeuAsnAsnGlyLeuLeuSerSerAspTyrValGluIle 180  
Db 704 AAATTCATTTTACCTCATACTGACCAATGATGTTGTGCTTCTGTATATGAGGATTT 763  
QY 181 HisTyrGluAsnGlyLysProGlnTyrSerLysGlyGlyLysCysTyrTyrHisGly 200  
Db 764 CACTACGAAATGGAAGAACCAAGACTTAAAGGTGGAAGAGCACTGTTACTACCATGGA 823  
QY 201 SerIleArgGlyValLysAspSerLysValAlaLeuSerThrCysAsnGlyLeuHisGly 220  
Db 824 AGCATCAGAGCGCGCAAGACTCCAGAGTGTGCTGCAACCTGCAATGAGACTTCATGCG 883  
QY 221 MetPheGluAspAspThrPheValTyrMetIleGluProLeuGlnLeuValHisAspGlu 240  
Db 884 ATGTTTAAAGATGATACCTTCTGCTATATATATAGAGCACTAGAGCTGATCATGATGAG 943  
QY 241 LysSerThrGlyArgProHisIleIleGlnLysThrLeuAlaGlyGlnTyrSerLysGln 260  
Db 944 AAAAGCAGAGGTGACACCATATATATCAAGAAACCTTGGCAGAGCAGTATTTCAACAA 1003  
QY 261 MetLysAsnLeuThrMetGluArgGlyAspGlnTrpProPheLeuSerGluLeuGlnTrp 280  
Db 1004 ATGAAGAATCTCACTATGGAAGAGGTGACCAGTGGCCCTTCTCTGATTAATACAGTGG 1063





Db	224	ATGCAAGCCGCCCGGACAGCAAGCTGGCGGACAGCGCCCTGGCGGGCTGCACACCTTGGCGGC	283
OY	21	AlaSerCysGlyProGlnArgGlyProAlaGlySerValProAlaSerAlaProAlaArg	40
Db	284	GCCTCTGGCGGCCCCCAAGCGGCGCCGCGGCTGGCTCCAGCGCCCGCGCCGC	343
OY	41	ThrProCysArgLeuLeuLeuValLeuLeuLeuLeuProProLeuAlaAlaSerSer	60
Db	344	ACGCGCGCCCTGGCGCTGCTTCGTCGCTTCCTCTGCTGCTGCTGCGCGCTGCTGC	403
OY	61	ArgProArgAlaTPrpGlyAlaAlaAlaProSerAlaProHisrPrpAsnGluTPrpAlaGlu	80
Db	404	CGGCCCCGCGGCGTGGGGGGCTGCTGGCCCCAGCGCTCCGATTGCATGAACCTGGAGAA	463
OY	81	LysAsnLeuGlyValLeuAlaAspGluAspAsnThrLeuGlnGlnAsnSerSerAsn	100
Db	464	AAAAATTTTGGAGTCTGGCAGATGAAGCAATATCTCCACAGAAATAGCACACTAAT	523
OY	101	IleSerTyrSerAsnAlaMetGlnLysGluIleThrLeuProSerArgLeuIleTyr	120
Db	524	ATCAGTTACAGCAATCCATGCAGAAAGAAATCCACTGCTTCAGACCTCAATATTTAC	583
OY	121	IleAsnGlnAspSerGluSerProTyrHisValLeuAspThrLysAlaIghisGlnGln	140
Db	584	ATCAACCAAGACTCGGAAAGCCCTTATCAGTTCCTGCACAAAGCCAGACACCAACAA	643
OY	141	LysHisAsnLysAlaValHisLeuAlaGlnAlaSerPheGlnIleGluAlaPheGlySer	160
Db	644	AAACATANTAAAGGCTGCTCATCTGGCCCCAGGCAAGCTTCCAAATTTGAACCTTGGCTCC	703
OY	161	LysPheIleLeuAspLeuIleLeuAsnAsnGlyLeuLeuSerSerAspTyrValGluIle	180
Db	704	AAATTCATCTTGGACCTCATATCGAAACATGCTTTGTTGCTTCGTGATTAATGGAGATT	763
OY	181	HisTyrGluAsnGlyLysProGlnTyrSerLysGlyGluHisCysTyrTyrHisGly	200
Db	764	CACCTCGAAATGGGAACACACAGTACTCTAAGGCTGGAGACACTGTTACATCAATGGA	823
OY	201	SerIleArgGlyValLysAspSerLysValAlaLeuSerThrCysAsnGlyLeuHisGly	220
Db	824	AGCATCAAGGCGTCAAAAGACTCCAAAGGCGCTCTGCACACTGCATGGACTTCATGCG	883
OY	221	MetPheGluAspAspThrPheValTyrMetIleGluProLeuGlnLeuValHisAspGlu	240
Db	884	ATGTTTGAAGATGATACCTCTGCTGTATATGATAGAGCCACATGACACTGGTTCATATGAG	943
OY	241	LysSerThrGlyArgProHisIleIleGlnLysThrLeuAlaGlyIleTyrSerLysGln	260
Db	944	AAAAGCAAGGTCGACACCATATATATCCAGAAACCTTGGCAGACAGTATTCTAAGCA	1007
OY	261	MetLysAsnLeuThrMetGlnArgGlyAspGlnTPrpPheLeuSerGluLeuGlnTPrp	280
Db	1004	ATGAGAAATCTCACACTATGGAAGAGGATGACAGTGGCCCTTCTCTCGAATTACAGTGG	1063
OY	281	LeuLysArgArgLysArgAlaValAsnProSerArgGlyIlePheGlnGluMetLysTyr	300
Db	1064	TTGAAAGAAAGAGAGAGAGAGTGCATCCACTGGTATATTGGAAGAAATGAATAAT	1123
OY	301	LeuGluLeuMetIleValAsnAspHisLysThrTyrLysLysHisArgSerSerHisAla	320
Db	1124	TTGGAACTTATGATTTGTAATGATCACAAAACGTATAAGAGCAATCCGCTTTCATATCA	1183
OY	321	HisThrAsnAsnPheAlaLysSerValValAsnLeuValAspSerIleTyrLysGlnGln	340
Db	1184	CATACCAACAACCTTGGCAAGTCCGTGTCACTTGTGGATTCTATTATTCAGAGAGAGAG	1243
OY	341	LeuAsnThrArgValValLeuValAlaValGluThrTPrpThrGluLysAspGlnIleAsp	360
Db	1244	CTCAACACCGAGGCTTCTCGTGGCTGTAGAGACCTGGACTGAGAGAGATCAGATTGAC	1303
OY	361	IleThrThrAsnProValGlnMetLeuHisGlnPheSerLysTyrArgGlnArgIleLys	380
Db	1304	ATCAACCAACACCTTGTGCAGATGCTCCATGATGTTCTCAAAAATCCGCGACCGCATTTAAG	1363

QY	381	GLHISALASPVALVALHISLEULISESERAIRVALTHPHEHISTYRLYSATGSErSer	400
Db	1364	CACCATGCTATGCTGTGCACCCATCTCCGGGTGCATTTCACATTAAGAACACAGT	142
QY	401	LEuSETpYrPHeGlyGlyVALcYSSerArgThArgGLyAlGLyAlAsnGLuTYrGLY	420
Db	1424	CTGAGTTACTTTCGAGGTGTCTCTTCTCCGACAAAGAGAACTTGGTCGTGAATGAGTATGGT	148
QY	421	LEuPROMETALVALALAGIVALILEuSERGLuSERLEuNALAGINSLEuGLYLIEGLN	440
Db	1484	CTTCCATGCGCATGGCAGCAAGATATTATCGACAGCGCTGGCTCAAAACCTGGAAATCCAA	154
QY	441	TYRGLuPROSErSERArgLYSPOLYScYASPCYSThGLuSETrPGLYGLYcYSILIE	460
Db	1544	TGGGAACCTTCTTAGCGAAAGGCCAAAATGACTGACAGAAATCCGGGGTGGCTCCATTC	160
QY	461	METGLuGLUTHRGLYVALSERHISSErArgLYSPHESerLYSCYSSErILEuGLUUTYR	480
Db	1604	ATGAGAGAAACAGGGGTGTCCCACTTCCTCCGAATTTTCCAAGTGCAGCATTTTGCAGCTAT	166
QY	481	ARGASPHeLEuGLuNArgGLYGLYGLYALAcYSLeuPHeASnArgPROThrLYSLeuPHe	500
Db	1664	AGGAGCTTTTTCACGAGAGAGGTGCAGGCTCGCTTTTTCACACAGGCCCAAAAGCTATATT	172
QY	501	GLUPROThrGLUCYSGLYASnGLYTYRVALGLVALAGLVLGLuGLUCYSPCYSGLYPHe	520
Db	1724	GAGCCACGGGAATGTGGAAATGGATACGTGCGAAGCTGGGGAGAGAGTGTATGTGGTTTTT	178
QY	521	HISVALGLUCYSTYRGLYLeuCYSCYSLYLYSCYSErLEuSERASnGLYALHISCYs	540
Db	1784	CATGTGGAAATGCTATGGATTATGCTGTAAAGAAATGTCCCTCCACACGGGGCTCACTGC	184
QY	541	SErASpGLyPROCYSCYsASnAnThrSERCYSLeuPHeGLUPROArgGLYTYRGLUCYS	560
Db	1844	ACGAGACGGGCCCTCGCTGAACAATACCTCATGTCTTTTCCACCCACGAGGATATAATGC	190
QY	561	ARGASPALVALASnGLUCYsAspIleThrGLUTYRCYSThGLYASPSerGLYGLINCYS	580
Db	1904	CGGGATGCGTGAACAGACGTGATATTACTGAATATTGACTGAGAGACTCTGTCAGTGC	196
QY	581	PROProASnLEuHISLYSGlINSpGLYTYRVALCYsASnGLINSnGLYARGCYSTYR	600
Db	1964	CCACCAAACTTTCATTAAGCAACACCGGATATGATGCATCAAAATCCAGGCCCGCTGCTAAC	202
QY	601	ASnGLYGLUCYsLYSThArgASpASnGLINCYSGLUTYRIleTrpGLYThLYSALALa	620
Db	2024	AATGGCGAGGTGCAMACACAGAACACAGTCTCACTCCATCTGGGAAACAAAGCTGCA	208
QY	621	GLYSErASpLYSPHeCYSTYRGLUYSLEuASnThrArgLUGLYThGLULYGLYASnCYs	640
Db	2084	GGGTGTGACAACTTCTGCTATTAAGAAGCTGAATACAGAAAGCACTGAAGAGGAAACATGC	214
QY	641	GLYLYSAspGLYASpArgTrpLIEGLINCYSSErLYSHIASpVALPHCYSGLYPHeLEu	660
Db	2144	GGGAAGATGACAGACCGGTGATTCAAGCAAAACATGATGTGTCTGGCATTTCTTA	220
QY	661	LEuCYSThRrASnLEuThArgALePROArgLIEGLYGLINSnGLYGLULIEleIRO	680
Db	2204	CTGTGTACCATTCTTACTCGAGCTCCACGTATTGTCAACTTCAAGGGGAGATATATCCA	226
QY	681	ThrSErPHeTYRHisGLINGLYArgVALILEASPCYSErGLYALAHISVALILEuASp	700
Db	2264	ACTTCCTCTCTACCATCAAGGCCGGGTGATTGACTGCAGTGTGCCCATGTAGTTTATGAT	232
QY	701	ASPAsPTrrASpVALGLTYRVALGLINSpGLYThrPROCYSGLYPROSErMeTHECYs	720
Db	2324	GATGATACGAGTGTGGGCTATGTAGAGATGGAAGCGCATGTGGCCCTCATATGATGTCT	238
QY	721	LEuASpArgLYSCYsLEuGLINLIEGLNALALEuASnMETSErCYSPROLEuASPSer	740
Db	2384	TTTAATATCGGAAGTGCCTAACAAATCCAAAGCCCTTAATATGAGACACTGTCCACCTGGATTCC	244

OY 741 LysGlyLysValCysSerGlyHisGlyValCysSerAsnGlnAlaThrCysIleCysAsp 760  
|||||  
Db 2444 AAGGTTAAAGTCTGTCGGGCGCATGGGCTGTAGTAATGAAGCCACCTGATTTGTGAT 2503  
OY 761 PheThrTrpAlaGlyThrAspCysSerIleArgAspProValArgAsnLeuHisProPro 780  
|||||  
Db 2504 TTCACCTGGGAGGAGGAGATTGACGTATCCGGGATCCAGTTAGGAACCTTCACCCGCC 2563  
OY 781 LysAspGlnGlyProLysGlyProSerAlaThrAsnLeuIleIleGlySerIleAlaGly 800  
|||||  
Db 2564 AAGGATGAAGGAGCCCAAGGCTCTAGTGCACCAATCTATATAGCTCCATCGCTGGT 2623  
OY 801 AlaIleLeuValAlaAlaIleValLeuGlyGlyThrGlyTrpGlyPheLysAsnValLys 820  
Db 2624 GCCATCCGTGTAGACAGTATTTGCTCTGGGGGACACAGCGTGGGATTTAAATGTCAAG 2683  
OY 821 LysArgArgPheAspProThrGlnGlnGlyProIle 832  
Db 2684 AAGAGAGGTTGATCTGATCTACAGCAAGGCCCATC 2719

## RESULT 6

US-60-324-185-1573

Sequence 1573, Application US/60324185

GENERAL INFORMATION:

APPLICANT: Morris, MacDonald

APPLICANT: Lal, Preeti

TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING

TITLE OF INVENTION: POLYMORPHISM SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE

TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY

FILE REFERENCE: GX-0019-1 P

CURRENT APPLICATION NUMBER: US/60/324,185

NUMBER OF SEQ ID NOS: 35862

SOFTWARE: PERL Program

SEQ ID NO 1573

LENGTH: 6400

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc. feature

OTHER INFORMATION: Incyte ID No: 037502.4

US-60-324-185-1573

## Alignment Scores:

Pred. No.:	1-09e-301	Length:	6400
Score:	4553.00	Matches:	832
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
	76	Gaps:	0

US-09-634-252a-4 (1-832) x US-60-324-185-1573 (1-6400)

OY 1 MetLysProProGlySerSerSerArgGlnProProLeuAlaGlyCysSerLeuAlaGly 20  
|||||  
Db 224 ATGAAGCGCGCGGAGCAGCTGCGGCGCGCGCGCTGCGGCGGAGCGCTGTCGCGC 283  
OY 21 AlaSerGlyProGlnArgGlyProAlaGlySerValProAlaSerAlaProAlaArg 40  
|||||  
Db 264 GCTTCTCTGGGCGGCGGCGGCGGCGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGG 343  
OY 41 ThrProProCysArgLeuLeuLeuValLeuLeuLeuProProLeuAlaAlaSerSer 60  
|||||  
Db 344 ACGCGCGCGCTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 403  
OY 61 ArgProAlaGlyArgGlyAlaAlaAlaProSerAlaProHisTrpAsnGlnThrAlaGlu 80  
|||||  
Db 404 CGGCGCGCGCGCTGCGGCGGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 463  
OY 81 LysAsnLeuGlyValLeuAlaAspGluAspAsnThrLeuGlnGlnAsnSerSerSerAsn 100  
|||||  
Db 464 AAAAATTTGGGAGTCTGCGGAGATGAAGACATTAATGCAACAGATAGACAGCGTAAAT 523

OY 101 IleSerTrpSerAsnAlaMetGlnLysGlnIleThrLeuProSerArgLeuIleTrpTrp 120  
|||||  
Db 524 ATCAGTTACAGCAATGCAATGCAAGAAATCACTGCTTCAAGCTCATATATTAC 583  
OY 121 IleAsnGlnAspSerGlySerProTrpHisValLeuAspThrLysAlaArgHisGln 140  
|||||  
Db 584 ATCAACCAAGACATCGGAACCCCTTATCAGCTTCTGACAAAGCAAGCACACAGCA 643  
OY 141 LysHisAsnLysAlaValHisLeuAlaGlnAlaSerPheGlnIleGlnAlaPheGlySer 160  
|||||  
Db 644 AACATATATAGGCTGTCCATCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 703  
OY 161 LysPheIleLeuAspLeuIleLeuAsnAsnGlyLeuLeuSerSerAspTrpValGlnIle 180  
|||||  
Db 704 AAATTCATTTCTGACCTCATCTGACAAATGCTTTGTTGCTTCTGCTGATTAATGAGATT 763  
OY 181 HisTrpGlnAsnGlyLysProGlnTrpSerLysGlyGlnHisCysTrpTrpHisGly 200  
|||||  
Db 764 CACTACGAAATGGAACACACAGTACTTAAGGCTGAGAGCACTGTACTACCATGCA 823  
OY 201 SerIleArgGlyValLysAspSerLysValAlaLeuSerTrpCysAsnGlyLeuHisGly 220  
|||||  
Db 824 AGCATCAGAGGCGTCAAGACTCCAGAGTGGCTGTCAACTCCAAATGAGACTTCATGCG 883  
OY 221 MetPheGluAspAspThrPheValTrpMetIleGluProLeuGlnLeuValHisAspGlu 240  
|||||  
Db 884 ATGTTTAACATGATGATCTGCTGCTATATGATATAGGCACAGTACAGCTGCTCATGATG 943  
OY 241 LysSerThrGlyArgProHisIleIleGlnLysThrLeuAlaGlyGlnTrpSerLysGln 260  
|||||  
Db 944 AAAAGCACAGCTGCACCATATATATCCAGAAACCTTGGCGAGACAGTATTTCAAGCAA 1003  
OY 261 MetLysAsnLeuThrMetGluArgGlyAspGlnTrpProPheLeuSerGlnLeuGlnTrp 280  
|||||  
Db 1004 ATGAGATCTCAGTATGGAAGAGGTGACAGTGGCTTCTCTCTGAAATTCAGTGG 1063  
OY 281 LeuLysArgArgLysArgAlaValAsnProSerArgGlyIlePheGlnGlnMetLysTrp 300  
|||||  
Db 1064 TTGAAAGAAAGAAAGAGAGCAGTGAATCCATCAGCTGATATTGGAAGAAATGAATAT 1123  
OY 301 LeuGlnLeuMetIleValAsnAspHisLysThrTrpLysLysHisArgSerSerHisAla 320  
|||||  
Db 1124 TTGGAATTTATGATTTGTAATGATCACAAACGTAATAAGAGCATCGCTTCTCATGCA 1183  
OY 321 HisThrAsnAspPheAlaLysSerValValAsnLeuValAspSerIleTrpLysGlnGln 340  
|||||  
Db 1184 CATACCAACAACCTTGGCAAGTCCGTGCTCAACCTTGTGATTTATTAACAGGACAG 1243  
OY 341 LeuAsnThrArgValValLeuValAlaValGlnTrpTrpTrpGlnLysAspGlnIleAsp 360  
|||||  
Db 1244 CTCACACACAGGCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1303  
OY 361 IleThrThrAsnProValGlnMetLeuHisGlnPheSerLysTrpArgGlnArgLys 380  
|||||  
Db 1304 ATCAACCAACAACCTTGGAGATCTCCATGAGTTCTCAAAATACCGGACACCGCATTAAG 1363  
OY 381 GlnHisAlaAspAlaValHisLeuIleSerArgValThrPheHisTrpLysArgSerSer 400  
|||||  
Db 1364 CAGATCTCTATGCTGTGCACCTCATCTCGGAGTGCATTTCACTATTAAGAGAGCGT 1423  
OY 401 LeuSerTrpPheGlyGlyValCysSerArgTrpArgGlyValGlyValAsnGlnTrpGly 420  
|||||  
Db 1424 CTGAGTTACTTTGGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1483  
OY 421 LeuProMetAlaValAlaGlnValLeuSerGlnSerLeuAlaGlnAsnLeuGlyIleGln 440  
|||||  
Db 1484 CTTCATATGCGAGGCGCAAGATATTATCGAGAGCCCTGCGTCAAAACCTTGGATCAAA 1543  
OY 441 TrpGlnProSerSerArgLysProLysCysAspCysTrpGlnSerTrpGlyGlyCysIle 460  
|||||  
Db 1544 TGGGAACCTTCTAGCAAGAAAGCCAAATGTGATGCAACAGATCTGGGCTGCTGCAATC 1603

QY 461 MetGluGluThrGlyValSerHisSerArgLysPheSerLysCysSerIleGluGluTyr 480  
DB 1604 ATGGAGGAAACAGGGGCTGCCATTTCTCGAAATTTTCAAGATGTCACATTTTGGAGTAT 1663  
QY 481 ArgAspPheLeuGlnArgGlyGlyValAlaCysLeuPheAsnArgProThrLysLeuPhe 500  
DB 1664 AGAAGCTTTTACAGAGAGAGGGGAGCCCTTTTCAACAGCCCAACCAACTATTTT 1723  
QY 501 GluProThrGlyCysGlyAsnGlyTyrValGluAlaGlyGluGlyCysAspCysGlyPhe 520  
DB 1724 GAGCCCAAGCAATGCAAAATGATAGCTGGAACTGGGAGGAGTGATGGATTTT 1783  
QY 521 HisValGluCysTyrGlyLeuCysCysLysCysSerLeuSerAsnGlyAlaHisCys 540  
DB 1784 CATGTGGAATGCTATGTATGCTGTAAGAAATGTTCCCTCTCCAAAGGGGGCTCACTGC 1843  
QY 541 SerAspGlyProCysCysAsnAsnThrSerCysLeuPheGlnProArgGlyTyrGluCys 560  
DB 1844 AGCAGCGGGCCCTGTAACAAATACCTCATGCTTTTTCAGCCCAAGGGGTATGATATGC 1903  
QY 561 ArgAspAlaValAsnGluCysAspIleThrGluTyrCysThrGlyAspSerGlyGlnCys 580  
DB 1904 CGGGATGCTGTGAACGAGTGTGATATTTCTGATATTTGCTGGAGACTCTGTCAGTGC 1963  
QY 581 ProProAsnLeuHisLysGlnAspGlyTyrAlaCysAsnGlnAsnGlnGlyArgCysTyr 600  
DB 1964 CCACCAAACTTTCATTAACCAAGACGAGATGTCATGCAATAAAATCAGAGCGCGCTGCATC 2023  
QY 601 AsnGlyGluCysLysThrArgAspAsnGlnCysGlnTyrIleTyrGlyThrLysAlaAla 620  
DB 2024 AATGGCGAGTGCACAAACAGACAGACACAGTGTCTGATCTGGGGACAAAGGCTGCA 2083  
QY 621 GlySerAspLysPheCysTyrGlyLysLeuAsnThrGluGlyThrGluLysGlyAsnCys 640  
DB 2084 GGGTCTGACAAATGCTGTATGTAAGAGCTGATACAGAAAGCAGTGAAGGAGGAACTGC 2143  
QY 641 GlyLysAspGlyAspArgTyrIleGlnCysSerLysHisAspValPheCysGlyPheLeu 660  
DB 2144 GGGAGAGATGAGAGCGGCTGATGTCAGTCCAGCAAAATGATGTTCTGTCGATGTTCTTA 2203  
QY 661 LeuCysThrAsnLeuThrArgAlaProArgIleGlyGlnLeuGlnGlyIleIlePro 680  
DB 2204 CTCTGACCAATCTTACTGACCTCCAGCTATTTGGTCAACTTCAGGGTGAATCTTCCA 2263  
QY 681 ThrSerPheTyrHisGlnGlyArgValIleAspCysSerGlyAlaHisValIleAsp 700  
DB 2264 ACTTCTCTTACCATCAACAGCGGGGATGTAAGTCACTGAGTGGCCCATTTAGAT 2323  
QY 701 AspAspThrAspValGlyTyrValGluAspGlyThrProCysGlyProSerMetMetCys 720  
DB 2324 GATGATACCGATGTGGGCTATGTAAGATGGAACCCCATGTGGCCGCTATGATGTGT 2383  
QY 721 LeuAspArgLysCysLeuGlnIleGlnAlaLeuAsnMetSerSerCysProLeuAspSer 740  
DB 2384 TTATGATCGAATGCTCTACAAATTCAGCCCTTAATATGACAGCTGTCTCACCTGATTC 2443  
QY 741 LysGlyLysValCysSerGlyHisGlyValCysSerAsnGluAlaThrCysIleCysAsp 760  
DB 2444 AAGGGTAAAGTCTGTTCCGGGCCATGGGGTGTATGTAAGTAAGCCACTGCAATTTCTGAT 2503  
QY 761 PheThrTTrpAlaGlyThrAspCysSerIleArgAspProValArgAsnLeuHisProPro 780  
DB 2504 TTCACCTGGGACAGGAGAGATTCAGATTCGCGGATTCAGATTCAGAACTTCACCCCCC 2563  
QY 781 LysAspGluGlyProLysGlyProSerAlaThrAsnLeuIleIleGlySerIleAlaGly 800  
DB 2564 AAGGATGAGAGACCAAGGCTCTAGTGCACCAATCTCTAATATAGCTTCATCCCTGCT 2623  
QY 801 AlaIleLeuValAlaAlaIleValLeuGlyGlyThrGlyTyrPheLysAsnValLys 820  
DB 2624 GCCATCTCTGTACAGCTATTTGCTTGGGGGACAGAGGCTGGGATTTAAATAATGTCAAG 2683  
QY 821 LysArgArgPheAspProThrGlnGlnGlyProIle 832

DB 2684 AAGAGAGGTTGCTGCTCTACTACGACAGGCCCATC 2719  
RESULT 7  
US-60-172-360-21719  
: Sequence 21719, Application US/60172360  
: GENERAL INFORMATION:  
: APPLICANT: Morris, MacDonald  
: APPLICANT: Lai, Preclt  
: TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using  
: FILE REFERENCE: GX-0007 P  
: CURRENT APPLICATION NUMBER: US/60/172,360  
: NUMBER OF SEQ ID NOS: 29838  
: SOFTWARE: PERL Program  
: SEQ ID NO 21719  
: LENGTH: 6391  
: TYPE: DNA  
: ORGANISM: Homo sapiens  
: FEATURE:  
: NAME/KEY: misc.feature  
: OTHER INFORMATION: Incyte ID No: 037502.4  
: NAME/KEY: unsure  
: LOCATION: 4043-4060, 4177, 4359, 4494  
: OTHER INFORMATION: a, t, c, g, or other  
US-60-172-360-21719  
Alignment Scores:  
Pred. No.: 2,86-301 Length: 6391  
Score: 4547.00 Matches: 831  
Percent Similarity: 99.88% Conservative: 0  
Best Local Similarity: 99.88% Mismatches: 1  
Query Match: 99.87% Indels: 0  
DB: 61 Gaps: 0  
US-09-634-252a-4 (1-832) x US-60-172-360-21719 (1-6391)  
QY 1 MetLysProProGlySerSerSerArgGlnProProLeuAlaGlyCysSerLeuAlaGly 20  
DB 224 ATGAGCGCGCCCGGAGCAGCTCGCGGCGCAGCCCGCGGCGCTGCAAGCTTGGCGGC 283  
QY 21 AlaSerCysGlyProGlnArgGlyProAlaGlySerValProAlaSerAlaProAlaArg 40  
DB 284 GCTTCTCGGCGCCCAACAGCGGCGGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 343  
QY 41 ThrProProCysArgLeuLeuLeuValLeuLeuLeuLeuProProLeuAlaSerSer 60  
DB 344 AGCGCGCCCTGGCGGCTGCT 403  
QY 61 ArgProArgAlaTrrGlyAlaAlaAlaProSerAlaProHisTrrAsnGluThrAlaGlu 80  
DB 404 CGGCCCGCGCGTGGGGGCTGCTCTCGCCGACGCTCGCATTTGGAATGAATGACAGAA 463  
QY 81 LysAsnLeuGlyValLeuAlaAspGluAspAsnThrLeuGlnGlnAsnSerSerAsn 100  
DB 464 AAAAATTTGGAGTCTGCGAGATGACATTAATTCGAACAAATATGACGACGATAT 523  
QY 101 IleSerTyrSerAsnAlaMetGlnLysGluIleThrLeuProSerArgLeuIleTyrTyr 120  
DB 524 ATCAGTACAGCAATGCAATGCAAGAAATACACACTGCTTCAAGACTCATATATATAC 583  
QY 121 IleAsnGlnAspSerGluSerProTyrHisValLeuAspThrLysAlaArgHisGlnGln 140  
DB 584 ATCAACCAAGACTCGGAAGCCCTTATCAAGTCTTGACCAAGGACAGACACAGCA 643  
QY 141 LysHisAsnLysAlaValHisLeuAlaGlnAlaSerPheGlnIleGluAlaPheCysSer 160  
DB 644 AAACATTAATTAAGGCTGCTCTCTGCGCCAGGCAAGCTTCACATTAACCTTGGCTCC 703  
QY 161 LysPheIleLeuAspLeuIleLeuAsnAsnGlyLeuLeuSerSerAspTyrValGluIle 180

|||||  
Db 704 AATTCATTCCTTGACCTCACTGAAACAAGGTTGTGTCTCTGATTAATGAGAAATT 763  
OY HISYRGVLAASNGLYLSPROGINTYRSELYSGLYGILUNHISCTYTRYTHISGLY 200  
Db 764 CACTACGAAATGGGAAACACAGTACTCTAAGGGGTGAGAGACACTTCTACCAATGCA 823  
OY SerLEIleargLYValLysaspSerLYsValAlaLeuSerThrCysasnGLYLeuHISGLY 220  
Db 824 AACATCAGAGCGGCTCAAAAGACTCCAGAGGTGGCTCTGCAACCTGCATATGACCTTCATGGC 883  
OY MetPheGLIAspAspThrPheValIYrMetILEGLIProLeuGLIleuValHISAspGLU 240  
Db 884 ATGTTTGAAGATGATACCTTCGTGATATGATAGACCACCTAGAGCTGGCTTCATGATGAG 943  
OY LysSerThrGLYArgProHISILEIleGLINLysThrLeuValGLYINTYRSELYSGILN 260  
Db 944 AAAAGACAGAGGTGCACACATATATCCAGAAAACCTTGGCAGACAGTATTTCAKCA 1003  
OY 261 MetLYsAsnLeuThrMetGLIArgGLYAspGLITrPProPheLeuSerGLIleuGLITrP 280  
Db 1004 ATGAAGAATCTCACTATGGAAGAGGTGACCAAGTGGCCCTTCTCTGAATTAACAATGG 1063  
OY 281 LeuLYsArgArgLYsArgAlaValAsnProSerArgGLYIlePheGLIleuMetLYsTYR 300  
Db 1064 TTGAAAAGAGAGAGAGACAGTGAATCCATCCAGTGTATATTGAAAGAAATGAATAT 1123  
OY 301 LeuGLIleuMetILEValAsnAspHISLYSThrTYLysLYsHISArgSerSEHISAla 320  
Db 1124 TTGGAACCTATGATGTTGTTAATGATCAAAAGCTATTAAGAAAGTCCCTTCTCAAGCA 1183  
OY 321 HISThrAsnAspPheAlaLYsSerValValAsnLeuValAspSerILETYRGLYGLIN 340  
Db 1184 CATACCAACACACTTGGCAAGTCCCGTGCACACCTTGGATTCATTTACAAAGAACAG 1243  
OY 341 LeuAsnThrArgValValLeuValAlaValGLIThrTrPThrGLIulysAspGLINleAsp 360  
Db 1244 CTCACACACAGGGGTGTCTGTGGCTGTAGAGACCTGGACCTGAGAAAGGTACAGATGAC 1303  
OY 361 ILEThrThrAspProValGLINMetLeuHISGLIPheSerLYSThrArgGLINArgILELY 380  
Db 1304 ATCACCACCAACCCCTGTGCAGATGCTCCATGACTTCTCAAAATACCGGCGCATTAAG 1363  
OY 381 GLINHISAlaAspAlaValHISLeuILESerArgValThrPheHISTYRLYsArgSerSE 400  
Db 1364 CAGCATGCGATGCTGTGCACCTCACTCGCGGTGACATTCACATATAAGAACAGAGT 1423  
OY 401 LeuSerTYRPhEGLYGLYValCysSerArgThrArgGLYValGLYAlaAsnGLITrTYRGLY 420  
Db 1424 CTGAGTTACTTTGGAGGTGTCTGTCTCCACAAAGAGAGTGTGTGAATGAGTAAGT 1483  
OY 421 LeuProMetAlaValAlaGLINValLeuSerGLINSerLeuAlaGLINAsnLeuGLYILEGLI 440  
Db 1484 CTTCCAATGGAGTGGCACAAAGATTATATCGCAGAGCTGGCTCAAAAACCTTGGAAATCA 1543  
OY 441 TrPGLIProSerSerArgLYsProlYSYsAspCysThrGLINuSerTrPGLIYGLYCYHILE 460  
Db 1544 TGGGAACCTTCTAGCAGAAAGCCAAAATGTGACTGCACAGAAATCCGGGGTGGCTGATC 1603  
OY 461 MetGLIleuThrGLYValSerHISSerArgLYsPheSerLYsCysSerILEleuGLITrTYR 480  
Db 1604 ATGGAGGAACAGGGGTGTCCCAATTCCTCGAAAATTTTCAAGAGCATTTTGGAAATAT 1663  
OY 481 ArgAspPheLeuGLINArgGLYGLYAlaCysLeuPheAsnArgPProThrLYsLeuPhe 500  
Db 1664 AGAGACTTTTACAGAGAGAGGTGAGCTGCTCTTTCACAGCGCCACAAAGCTATTTT 1723  
OY 501 GLIuProThrGLIulysGLYAsnGLYTrValGLIAlaGLYGLIulysAspCysGLYIlePhe 520  
Db 1724 GAGCCCCAGCAATGTGGAATGATGATCGTGAAGAGCTGGGAGAGAGTGTGATTTGGTTT 1783  
OY 521 HISValGLIulysTYRGLYleuCYsLYsLYsCysSerLeuSerAsnGLYAlaHISLYs 540  
|||||

Db 1784 CATGTGAAGTCTATGATTAATGCTGTAAGAATGTCCTCTCCACAGGGGCTCACTGC 1843  
OY 541 SerAspGLYProCysCysAsnAsnThrSerCysLeuPheGLINProArgGLYTYRGLYs 560  
Db 1844 AGCGAGGGGCGCTGTGTAAACATTAATCTCAATGTCTTTTCAAGCCAGAGGGTATAAATGC 1903  
OY 561 ArgAspAlaValAsnGLIulysAspPheThrGLITrTYRGLYsAsnGLIulysGLYs 580  
Db 1904 CGGATCGCTGTCAACAGATGTGATATCTGAATATTTGTACTGGAGACTGTGGTCAATGC 1963  
OY 581 ProProAsnLeuHISLYsGLINAspGLYTrValAlaCysAsnGLINAsnGLIulysTYR 600  
Db 1964 CCACCAATCTTCAATTAACCAAGAGGATATCATGCAATCAAAATCAGAGCGCGCTGATC 2023  
OY 601 AsnGLIulysCysLYsThrArgAspAsnGLINuSerGLITrILETrPGLIThrLYsAla 620  
Db 2024 AATGGCGAGTCAAGACCAAGACAGACAGTGTCTGATCATCTGGGGAACAAAGCTGCA 2083  
OY 621 GLYSerAspLYsPheCysTYRGLIulysLeuAsnThrGLIulysGLYAsnGLYs 640  
Db 2084 GGGTCTGACAGATTCTGCTATGAAAAGCTGAATACAGAAAGCACAGAGAGAAATGTC 2143  
OY 641 GLYLYsAspGLYAspArgTrPILEGLINuSerLYsHISAspValPheCysGLYIleu 660  
Db 2144 GGGAGGATGAGACCGGTGATTCAGTGCAGCAAAACATGATGTGTCTGTGATTCCTTA 2203  
OY 661 LeuCYSThrAsnLeuThrArgAlaProArgILEGLINleuGLINGLYIleTrPPro 680  
Db 2204 CTCTGTACCAATCTTACTCGAGCTCCACAGTATGTGTCAACTTTCAGAGGTGAGATCTTCCA 2263  
OY 681 ThrSerPheTYRHISGLINLYsArgValILEAspCysSerGLYAlaHISValLeuAsp 700  
Db 2264 ACTTCCTTCTACATCAAAAGCGGGTGTATGATGATGATGATGATGATGATGATGAT 2323  
OY 701 AspAspThrAspValGLYTrValGLIulysPGLIThrProCysGLYProSerMetCys 720  
Db 2324 GATGATACGGATGCGGTATGATAGAAATGGAAGCCCATGTGGCCCTCTATGATGTGT 2383  
OY 721 LeuAspArgLYsCysLeuGLINleuAlaLeuAsnMetSerSerCysProLeuAspSer 740  
Db 2384 TTACATGTGAAGTCTCTTAACAATTCAGCCCTTAATATAGACAGCTGTCCATTCATTC 2443  
OY 741 LysGLYLYsValCysSerGLYHISGLYValCysSerAsnGLIAlaThrCysILECysAsp 760  
Db 2444 AAGGTTAAAGTCTGTGGCGCATGGGTGTGTGATATGAAGCCACCTGCAATTTGTGAT 2503  
OY 761 PheThrTrPAlaGLIThrAspCysSerILEArgAspProValArgAsnLeuHISProPro 780  
Db 2504 TTCACTCGCGGAGAGACAGATTGAGATCCGGGATCCAGTTAGCAACCTTCACCCCCC 2563  
OY 781 LysAspGLIulysProlYSYsGLYProSerAlaThrAsnLeuILEIleGLYSerILEAGLY 800  
Db 2564 AAGATGAAGAGACCAAGAGGCTCTAGTCCCAATCTCATTAATATAGCTTCATCTGCTGT 2623  
OY 801 AlaILEuValAlaAlaILEValleuGLYGLYThrGLITrPGLIYPhelysAsnValLYs 820  
Db 2624 GCCATCTCGTAGAGAGATATGCTCTGGGGACAGAGCTGGGATTTAAAAATGTCAAG 2683  
OY 821 LysArgArgPheAspProThrGLINGLIYProILE 832  
Db 2684 AAGAGAGGTTCTGATCTACTACAGCAAGGCCCATC 2719  
RESULT 8  
US-60-213-359-127  
Sequence 127, Application US/60213359  
GENERAL INFORMATION:  
APPLICANT: Morris, MacDonald  
APPLICANT: Lal, Preeti  
APPLICANT: Diep, Dinh  
TITLE OF INVENTION: Method for the identification of sequence polymorphisms using  
TITLE OF INVENTION: Polynucleotide sequence databases, and single nucleotide poly  
FILE REFERENCE: GX-0015 P

CURRENT APPLICATION NUMBER: US/60/213, 359  
: CURRENT FILING DATE: 2000-06-21  
: NUMBER OF SEQ ID NOS: 7924  
: SOFTWARE: PERL Program  
: SEQ ID NO 127  
: LENGTH: 6401  
: TYPE: DNA  
: ORGANISM: Homo sapiens  
: FEATURE:  
: NAME/KEY: misc.feature  
: OTHER INFORMATION: Incyte ID NO: 037502.4  
: US-60-213-359-127

Alignment Scores:  
Pred. No.: 8,48e-301 Length: 6401  
Score: 4540.00 Matches: 832  
Percent Similarity: 99.88% Conservative: 0  
Best Local Similarity: 99.88% Mismatches: 0  
Query Match: 99.71% Indels: 1  
Gaps: 0

US-09-634-252a-4 (1-832) x US-60-213-359-127 (1-6401)

```
OY      1 MetlySPROPGlySerSerArgInProProLeuAlaGlyCysSerLeuAlaGly 20
Db      224 ATGAAGCCGCGCGAGCAGCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 283
OY      21 AlasercyGlyProGlnArgGlyProAlaGlySerValProAlaSerAlaProAlaArg 40
Db      284 GCTTCTCTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 343
OY      41 ThrProProCysArgLeuLeuLeuValLeuLeuLeuLeuProProLeuAlaAlaSerSer 60
Db      344 AGCGCGCGCGCGCGCGCGCGCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCG 403
OY      61 ArgProArgAlaTropGlyAlaAlaAlaProSerAlaProHisTrrpAsnGluTrrAlaGlu 80
Db      404 CCGCGCGCGCGCGCGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 463
OY      81 LysAsnLeuGlyValLeuAlaAspGluAspAsnThrLeuGlnGlnAsnSerSerSerAsn 100
Db      464 AAAAATTTGGAGTCTGCGCAGATGAAGCAATATTCACACAGCAATACAGCAGTAAT 523
OY      101 IleserTyrSerAsnAlaMetGlnGlnGluIleThrLeuProSerArgLeuIleTyrTyr 120
Db      524 ATCAGTTACAGCATCAATGCAAGAAAGAAATCACTGCTTCACAGCTCATATATATAC 583
OY      121 IleAsnGlnAspSerGluSerProTyrHisValLeuAspThrLysAlaArgHisGln 140
Db      584 ATCAACCAAGACTCGGAAGCCCTTATCAGTTCCTTGACACAAAGCAAGACACACAA 643
OY      141 LysHisAsnLysAlaValHisLeuAlaGlnAlaSerPheGlnIleGluAlaPheGlySer 160
Db      644 AAACATTAATTAAGCTGTCATCTGCGCCCAAGCAAGCTTCAGATGAAGCTTCGCTCC 703
OY      161 LysPheIleLeuAspLeuIleLeuAsnAsnGlyLeuLeuSerSerAspTyrValGlnIle 180
Db      704 AAATTTATTTTACCTCATCTGATCAATGAGTTTGTGTTCTTCTGATTATGTGCAAT 763
OY      181 HisTyrGlnAsnGlyLysProGlnTyrSerLysGlyGlnHisCysTyrTyrHisGly 200
Db      764 CATACGAAATATGGAAACACAGTACTTAAGGTGGAGGAGCTTTACTATACATGGA 823
OY      201 SerIleArgGlyValLysAspSerLysValAlaLeuSerThrCysAsnGlyLeuHisGly 220
Db      824 AGCATGAGGCGGCAAGCAAGCTCAAGGTGCTGTCAACCTCAATGAGCTTCATGAGC 883
OY      221 MetPheGlnAspSerThrPheValTyrMetIleGlnProLeuGlnLeuValHisAspGlu 240
Db      884 ATGTTTAAAGATGATACCTTCGTATATATGATAGACCACTAGAGCTGGTTCATGATAG 943
OY      241 LysSerThrGlyArgProHisIleIleGlnLysThrLeuAlaGlyGlnTyrSerLysGln 260
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Db      944 AAAACCAAGTCGACCAACATATATCCAGAAACCTTGGCAGGACAGTATCTAAGCAA 1003
OY      261 MetLysAsnLeuThrMetCylArgGlyAspGlnTrrProPheLeuSerGluLeuGlnTrr 280
Db      1004 ATGAAGAAATCTCATATGAGAAAGAGTGAACAGTGCGCTTCTCTCTGATATTAACAGTG 1063
OY      281 LeuLysArgArgLysArgAlaValAsnProSerArgGlyIlePheGlnLeuMetLysTyr 300
Db      1064 TTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1123
OY      301 LeuGlnLeuMetIleValAsnAspHisLysTrrTyrLysLysHisArgSerSerHisAla 320
Db      1124 TTGGAACCTTATGATTTGTAATGATCAAAAGCTATTAAGACATCGCTTCTCTCATGA 1183
OY      321 HisThrAsnAspPheAlaLysSerValAlaAsnLeuValAspSerIleTrrLysGlnGln 340
Db      1184 CATACCAACAACTTTGCCAAAGTCCGAGCAACCTTGATGATTTTATTAACAAGAGCGAG 1243
OY      341 LeuAsnThrArgValValLeuValAlaValGluThrTrrPheGlnLysAspGlnIleAsp 360
Db      1244 CTCACACACAGGTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1303
OY      361 IleThrThrAsnProValGlnMetLeuHisGluPheSerLysTyrArgGlnArgIleLys 380
Db      1304 ATCACCACCAACCTTGCAGATGCTCCATGAGTTCATAAATACCGCGCAGCCATTAG 1363
OY      381 GlnHisAlaAspAlaValHisLeuIleSerArgValThrPheHisTrrLysArgSerSer 400
Db      1364 CACATGCTGATGCTGCGACCTTCATCTCCGCGGTGACATTTACATTAAGAACACAGT 1423
OY      401 LeuSerTyrPheGlyGlyValLysSerArgThrArgGlyValGlyAlaAsnGluTyrGly 420
Db      1424 CTGAGTTACTTTGGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1483
OY      421 LeuProMetAlaValAlaGlnValLeuSerGlnSerLeuAlaGlnAsnLeuGlyIleGln 440
Db      1484 CTTCATATGCGACAGCGCAAGATATTAATGCGACAGCTTGCTCAAAACCTTGGATCCAA 1543
OY      441 TrrGlnProSerSerArgLysProLysCysAspCysThrGlnSerTrrGlyGlyCysIle 460
Db      1544 TGGCAACCTTCTAGACAAAGCCAAATGTGACGACAGATCTCGGGGGCTGCATC 1603
OY      461 MetGlnLeuThrGlyValSerHisSerArgLysPheSerLysCysSerIleLeuGlnTyr 480
Db      1604 ATGAGCAAGAAAGAGGAGTGCATTCGAAATTTCAAAATTCACACATTTTGGAGTAT 1663
OY      481 ArgAspPheLeuGlnArgGlyGlyValAcysLeuPheAsnArgProThrLysLeuPhe 500
Db      1664 AGAGACTTTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1723
OY      501 GlnProThrGlnCysGlyAsnGlyTyrValGlnAlaGlyGlnGlyCysAspCysGlyPhe 520
Db      1724 GAGCCACAGGAAATGTGAAATGATACGTGGAACCTGGGAGAGAGTGGATTTGCTTTT 1783
OY      521 HisValGlyCysTyrGlyLeuCysCysLysLysCysSerLeuSerAsnGlyAlaHisCys 540
Db      1784 CATGTGAAATCTTATGATTAATTCGTAAGAAATTTCCCTCTCCAAAGGGGCTCACAGTGC 1843
OY      541 SerAspCylProCysCysAsnAsnThrSerCysLeuPheGlnProArgGlyTyrGlyCys 560
Db      1844 AGCGACGCGCGCTGCTGTATCAATACCTCATGCTTTTAAAGCCACGAGGCTATGAATG 1903
OY      560 SArgAspAlaValAsnGlyCysAspIleThrGlnTyrCysThrGlnLysAspSerGlyGlnCys 580
Db      1904 CCGGAGATCTTGTGAAGAGAGTGTGATATTCAGAAATTTGTAAGTGTGAGCTGCTGCTG 1963
OY      580 SProProAsnLeuHisLysGlnAspGlyTyrAlaCysAsnGlnAsnGlnGlyArgCysTyr 600
Db      1964 CCCACCAATATCTTCAATAGCAAGAGCATATGCAATGCAAAATTCAGGGGCGCTGCTGA 2023
OY      600 rAsnGlyGlyCysLysTrrArgAspAsnGlnCysGlnTrrTrrPheGlyThrLysAlaAl 620
Db      2024 CAATGGCGAGTGCAAGACAGACAGACACACAGTGTGATGATCTGGGAGACAAAGGCTGC 2083
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QY 620 aglyseraspysphecystyrGluLysLeuasnThrGluGlyThrGluLysGlyAsnCy 640
DB 2084 AGGCTCTGCAAGTCTCTGTATGAAAGCTGATACAGAGAGACAGAGAGGAAACTG 2143
QY 640 sGlyLysaspGlyaspArgTrpIleGlnCysSerLysHisaspValPheCysGlyPhe 660
DB 2144 CGGGAGAGATGAGACCGGTGGATTGACAGCAAAACATGATGTCTGTGGATTCTT 2203
QY 660 uLeuCyThrAsnLeuThrArgAlaProArgIleGlnLeuGlnGluIleLeuIle 680
DB 2204 ACTGCTACCAATCTTACTCGAGCTCCACGATATGCTCAACTTCAGGGAGATCAATPCC 2263
QY 680 oThSerPheTrpHisGlnGlyArgValIleaspCysSerGlyAlaHisValValLeuAs 700
DB 2264 AACTTCCTTCTACATCAAGAGCCGGGTGATGTAGCTGATGCTGATGCTGATTTTACA 2323
QY 700 pAspAspThrAspValGlyTrpValGluAspGlyThrProCysGlyProSerMetMeCy 720
DB 2324 TGATGATACGGATGCGGTATGTAGAAATGAGAACGGCATGTGGCCCTGATGATGATG 2383
QY 720 sLeuAspArgLysCysLeuGlnIleGlnAlaLeuAsnMetSerSerCysProLeuAspSe 740
DB 2384 TTTACATCGGAAGTCTCTGAGCAATTCACCCCTTAATATAGAGAGCTGTCTCAGATC 2443
QY 740 rLysGlyLysValCysSerGlyHisGlyValCysSerAsnGluAlaThrCysIleCysAs 760
DB 2444 CAAGGTAAGTCTGTGGGGCATGGGTGTGTAGTATGAAGCCAGCTGCTTGTGGA 2503
QY 760 pPheThrTrpAlaGlyThrAspCysSerIleArgAspProValArgAsnLeuHisProPr 780
DB 2504 TTTCACTCGGCGAGGACAGATGTCAGTATCCGGGATCCAGTTAGGAACCTTCACCCCC 2563
QY 780 oLysaspGluGlyProLysGlyProSerAlaThrAsnLeuIleIleGlySerIleAlaG 800
DB 2564 CAAGATGAAGACCAAGGCTCTAGTCCACCAATCTCATATATAGGCTCCATCGCTG 2623
QY 800 yAlaIleLeuValAlaAlaIleValLeuGlyLysThrGlyTrpGlyPheLysAsnValLy 820
DB 2624 TGCCATCTCGTAGAGAGCATTTGCTCTTGGGGGACAGCTGGGGATTTAAAAATGTC 2683
QY 820 sLysArgArgPheAspProThrGlnGlnGlyProIle 832
DB 2684 GAAGAGAAAGTTGATCTCTACTACAGCAAGGCCCATC 2720

RESULT 9
US-09-760-484-15
: Sequence 15, Application US/09760484
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PT243
: CURRENT APPLICATION NUMBER: US/09/760,484
: CURRENT FILING DATE: 2001-01-16
: Prior application data removed - consult PALM or file wrapper
: NUMBER OF SEQ ID NOS: 638
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 15
: LENGTH: 4440
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (4149)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: SITE
: LOCATION: (4219)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: SITE
: LOCATION: (4341)
: OTHER INFORMATION: n equals a,t,g, or c
US-09-760-484-15

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## Alignment Scores:

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Pred. No.: 1,le-276 Length: 4440
Score: 4186.00 Matches: 759
Percent Similarity: 98.71% Conservative: 7
Best Local Similarity: 97.81% Mismatches: 10
Query Match: 91.94% Indels: 0
DB: 30 Gaps: 0

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US-09-634-252a-4 (1-832) x US-09-760-484-15 (1-4440)

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QY 57 AlAlaSerSerArgProArgAlaTrpGlyAlaAlaAlaProSerAlaProHisTrpAsn 76
DB 1 GCCGCCCTGCTCCGCCGCCGCCCTGGGGGGCTCTGCGCCACAGCTCCCATTTGGAT 60
QY 77 GluThrAlaGluLysAsnLeuGlyValLeuAlaAspGluAspAsnThrLeuGlnAsn 96
DB 61 GAACCTGCAGAAAAAATTTGGAGTCTTGCCATGAGACATACATTCACACAGAT 120
QY 97 SerSerSerAsnIleSerTrpSerAsnAlaMetGlnLysGluIleThrLeuProSerArg 116
DB 121 AGCAGCAGTAATATACATTACAGCAATGCAGAAAGAAATCACACCTGCTTCAAGA 180
QY 117 LeuIleTrpTrpIleAsnGlnAspSerGluSerProTrpHisValLeuAspThrLysAla 136
DB 181 CTCATATATTATACATCAACCAAGACTCGAAAGCCCTTATCAGTCTTGACACAAGACA 240
QY 137 ArgHisGlnGlnLysHisAsnLysAlaValHisLeuAlaGlnAlaSerPheGlnIleGlu 156
DB 241 AGACACGAGAAAAAATTAATTAAGCTGTCCATGTGGCCGAGAGCTTCCAGATTA 300
QY 157 AlaPheGlySerLysPheIleLeuAspLeuIleLeuAsnAsnGlyLeuLeuSerSerAsp 176
DB 301 GCCCTGGCTCCAAATTCATTCTTGACCTCATACTGAACAATGTTGTGTCTTCTGAT 360
QY 177 TrpValGluIleHisTrpGluAsnGlyLysProGlnTrpSerLysGlyGluHisCys 196
DB 361 TATGTGAGATTCCTCAAGAAATGAGAAACACAGTACTTAAGGGAGAGACACTGT 420
QY 197 TrpTrpHisGlySerIleArgGlyValLysAspSerLysValAlaLeuSerThrCysAsn 216
DB 421 TACTACCATGGAACATCAGAGCGCTCAAGACTCCAGAGTGGCTGTCTCAACCTGCAT 480
QY 217 GlyLeuHisGlyMetPheGluAspAspThrPheValTrpMetIleGluProLeuGluLeu 236
DB 481 GCACTTCATGCAATGTTGAAGATGATACCTTCGTATATGATAGAGCCATGAGACTG 540
QY 237 ValHisaspGluLysSerThrGlyArgProHisIleIleGlnLysThrLeuAlaGlyGln 256
DB 541 GTTCATGATGAGAAAGACAGAGTGCACACATTAATCCAGAAACCTTGGCAGAGACG 600
QY 257 TyrSerLysGlnMetLysAsnLeuThrMetGluArgGlyAspGlnTrpProPheLeuSer 276
DB 601 TATTTTACGAATAAGAGATCTACATATGGAAGAGGTGACCGTGGCTTTCTCTCT 660
QY 277 GluLeuGlnTrpLeuLysArgArgLysArgAlaValAsnProSerArgGlyIlePheGlu 296
DB 661 GAATTACAGTGGTTGAAGAAGACAGACAGCACTGATCATCAGCGGTGATTTTGA 720
QY 297 GluMetLysTrpLeuGluLeuMetIleValAsnAspHisLysThrTrpLysLysHisArg 316
DB 721 GAATGAATAATTTGGAACTTATGATGTTAATATATCAAAAGATTAAGAACATCGC 780
QY 317 SerSerHisAlaHisTrpAsnAsnPheAlaLysSerValValAsnLeuValAspSerIle 336
DB 781 TCTTCTCATGACACTTACCAACAATTTGCAAGTCCGTGCTGCACTTGTGATTTCTATT 840
QY 337 TrpLysGlnGlnLeuAsnThrArgValValLeuValAlaValGluThrTrpThrGluLys 356
DB 841 TACAAGAGCAGCTCAACACAGAGGTTGCTGCTGTGCTGAGAGACTGACAGAGAG 900
QY 357 AspGlnIleAspIleThrTrpAsnProValGlnMetLeuHisGluPheSerLysTrpArg 376
DB 901 GATCAGATTGACATCACCAACCCCTGTGATGCTCCATGATGATTCTCAAAATTACCGG 960

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[illegible]



Oy	168	LeuSnSnngLyleLeuLeuSerSerAspPyrValGluIleHISrYrGluAsnGlyPro	187
Db	412	CTGAACAAATGGTTTGGCTATCTTCTGACTAGCTGGAGATCCACTATGAAGAAGGGAAGAC	471
Oy	188	GlnTyrSerLysGlyGlyGluHisCysrYrThrHisGlySerIleArgGlyValLysAsp	207
Db	472	ATGTACTCTAAGGGGTGAGACACCTGTTACTACACCGAAGACATCAGAGCGTCAAGAT	531
Oy	208	SerLysValAlaLeuSerThrCysAsnGlyLeuHISGlyMetPheGluAspAspThrPhe	227
Dc	532	TCGAGGGGGCTCATCGACTGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG	591
Oy	228	ValTyrMetIleGluProLeuGluLeuValHisAspGlyLysSerThrGlyArgProHis	247
Db	592	GTCATATATGATAGAGACCTCTGGAACTGACTGATGATGAGAAAGACACGCGACACAC	651
Oy	248	IleIleGlnLysThrLeuAlaGlyGlnTyrSerLysGlnMetLysAsnLeuThrMetLys	267
Db	652	ATAATCCAGAAACCTTGGCGAGGACAGTATCTTAAGCAGATGAAGAATCTCAGACACAA	711
Oy	268	ArgGlyAspGlnTyrProPheLeuSerGluLeuGlnTyrPheLysArgArgLysArgGly	287
Db	712	GGCAGTGACCGTGGCTTCTGCTACCTGAATTTACAATGGCTGAGAGAAGAAAGAAAGAC	771
Oy	288	ValAsnProSerArgGlyIlePheGluGluMetLysTyrLeuGluLeuMetIleValAsn	307
Db	772	GTCATATCATCTCGTGGTGGTGTGAAGAAATGAAGTATTTGGAGCTTATGATTTGAT	831
Oy	308	AspHisLysThrLysLysLysHisArgSerSerHisAlaHisThrAsnAsnPheAlaLys	327
Db	832	GATACCAAGACGTTATGAAGAACACCGCTCTCTACAGCGGCTATCCACAACTTGGCAAG	891
Oy	328	SerValValAsnLeuValAspSerIleTyrLysGluGlnLeuAsnThrArgValValLeu	347
Db	892	TCTGTGGTCAACCTTGTAAGATTCTATTTACAGAGAACGCTCAACACCAAGGCTGTCTG	951
Oy	348	ValAlaValGluThrTyrThrGluLysAspGlnIleAspIleThrThrAsnProValGln	367
Db	952	GTGGCTGCGAGACCTGGACCGAAGAGATCACTTGCATCACCATCAACCCCGTGCAG	1011
Oy	368	MetLeuHISGluPheSerLysTyrArgGlnArgIleLysGlnHISAlaAspAlaValHis	387
Db	1012	ATGTACTACTGACTTCTCCAACTACCGGAGCGAATCAACAGCACGCTGACGCGTCCAC	1071
Oy	388	LeuIleSerArgValThrPheHisTyrLysArgSerSerLeuSerTyrPheGlyGlyVal	407
Db	1072	CTCATCTCTCGCGCGAGCATTCCTCATTTATGAAGAGACGCTGAGTACTTGGAGGCGTG	1131
Oy	408	CysSerArgThrArgGlyValGlyValAsnGluLysGlyLeuProMetAlaValAlaGln	427
Db	1132	TGTTCTGCAATTAAGAGGGGTGGTGGTGAATAGATGGTCTTCCAAATGGCGGTGCACAA	1191
Oy	428	ValLeuSerGlnSerLeuAlaGlnAsnLeuGlyIleGlnTyrPgluProSerSerArgLys	447
Db	1192	GTAATTATCAGAGACCTGGCTCAAAACCTTGGAAATCCAGTGGAAACCTTCAGCAGAGAG	1251
Oy	448	ProLysCysAspCysThrGluSerTyrPgluLysLysIleMetGluGluThrGlyValSer	467
Db	1252	CCAAAATGTGATCATAGACTCTCGGGGCGCTGCATCATGGAAGAAACAGGGGTGTCC	1311
Oy	468	HisSerArgLysPheSerLysCysSerIleLeuGlnTyrArgAspPheLeuGlnArgGly	487
Db	1312	CACCTCTCAAAAGTTCTCAAACTGCAGCATTTTGGAGTACAGAGACTTTTTCAGAGAGAT	1371
Oy	488	GlyGlyAlaCysLeuPheAsnArgProThrLysLeuPheGluProThrGluCysGlyValSn	507
Db	1372	GGCGGAGCATCTCTTTCAATAGGCAACACTAAAGCTTTTGAGCCACCAAGCAATGTGGAAAT	1431
Oy	508	GlyTyrValGluAlaGlyGluGluCysAspCysGlyPheHisValGluCysTyrGlyLeu	527
Db	1432	GGATATGTGGAGGCCGGGAGGAATGCCACTGTGTGTTCCATATGTGAATGCTATAGGACT	1491

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OY 528 CyscYsYsYsYsYsYsSerLeuSerAsnGlyAlaHisYsYsSerAspGlyProCysCysAsn 547
Db 1492 TGCTGTAGAAAGTGTGCCCTCTCCAAATGGGCCCACTGACAGACAGGCCCTCGTCTAAC 1551
OY 548 AsnThrSerCysLeuPheGlnProArgGlyTyrGlyCysArgAspAlaValAsnGlyCys 567
Db 1552 AACACCTCATGTCTTTTTTCAGTCACAGAGGGTATGATGTATCGGGATGCCGTAAACAGCTGT 1611
OY 568 AspIleThrGlnGlyTyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisYsGln 587
Db 1612 GATATCACCAGACTACTGCACTGGAAAGACTCTGGCCAGTGCACCCAGACCTTCATTAACAA 1671
OY 568 AspGlyTyrAlaCysAsnGlnAsnGlnGlyArgCysTyrAsnGlyGlyCysYsThrArg 607
Db 1672 GATGGCTATAGCTGATTCGAATCAAAATCAAGGGTGCCTGTCAAATGGCAGGATGCACAAG 1731
OY 608 AspAsnGlnCysGlnTyrIleThrGlyThrLysAlaAlaGlySerAspLysPheCysTyr 627
Db 1732 GACAATCATATCCCACTATCATCTGGGGGACAAAGGCTGGGGGTGCAGCAAGTTCGCTAT 1791
OY 628 GlyLysLeuAsnThrGlnGlyTyrHisLysGlyAsnCysGlyLysAspGlyAspArgTyr 647
Db 1792 GAAAGCTGACACCGGAAGGCCACCGAAGGCCATTTGTGAAAGATATGACACCGGTGG 1851
OY 648 IleGlnCysSerLysHisAspValPheCysGlyPheLeuLeuCysThrAsnLeuThrArg 667
Db 1852 ATCCCGTACACCAACATGATGTGTCTGTGGATTTCTGTGTCATTGGACCAATCTTACCGGA 1911
OY 668 AlaProArgIleGlyGlnLeuGlnGlyLysIleIleProThrSerPheTyrHisGlnGly 687
Db 1912 GCTCCACCTATTCGGTCAACTTCACAGAGAGATCAATCCGACTCTCTTATCATCAAAAGC 1971
OY 688 ArgValIleAspCysSerGlyAlaHisValValLeuAspAspAspThrAspValGlyTyr 707
Db 1972 CGAGTGATGTGACTGCAAGTGGTGCTCATGTATTTAGACGATGATACAGACTGGAGTTAC 2031
OY 708 ValGluAspGlyThrProCysGlyProSerMetMetCysLeuAspArgLysCysLeuGln 727
Db 2032 GTTGAAGATGGAGACATCCGTGTGGCCCTTCACAGATGCTCTTAAGATGGAGAGCCCTACAG 2091
OY 728 IleGlnAlaLeuAsnMetSerSerCysProLeuAspSerLysGlyLysValCysSerGly 747
Db 2092 ATTCAAGCCCTGCAATATATAGCAGCGCCCACTTGACTGATCAAGGGTAAAGTCTGCTCCGG 2151
OY 748 HisGlyValCysSerAsnGlnAlaThrCysIleCysAspPheThrTrpAlaGlyThrAsp 767
Db 2152 CACGGGGTGTGTAGCAACAGAAAGCCACCTGCATCTGTGATTTCACTTGGGACAGGCACAGAC 2211
OY 768 CysSerIleArgAspProValArgAsnLeuHisProProLysAspGlnGlyProLysGly 787
Db 2212 TGCACGATCCGGGATTCAGTTGTGGAAACCAACCCCTTAAGATGAAGGCCCTTAAGGCT 2271

RESULT 11
US-09-631-534-9
: Sequence 9, Application US/09631534
: GENERAL INFORMATION:
: APPLICANT: Sheppard, Paul O.
: APPLICANT: Baldwin, Nand
: APPLICANT: Delisher, Theresa A.
: APPLICANT: Bishop, Paul D.
: APPLICANT: Taft, David W.
: TITLE OF INVENTION: DISINTERGRIN HOMOLOGUE. MAHBP
: FILE REFERENCE: 98-2961
: CURRENT APPLICATION NUMBER: US/09/631,534
: CURRENT FILING DATE: 2000-08-03
: PRIOR APPLICATION NUMBER: 60/092,371
: PRIOR FILING DATE: 1998-07-10
: PRIOR APPLICATION NUMBER: 60/147, 410
: PRIOR FILING DATE: 1999-08-05
: PRIOR APPLICATION NUMBER: 09/351,414
: PRIOR FILING DATE: 1999-07-09
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: FASTSEQ for Windows Version 3.0

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SEQ ID NO 9  
LENGTH: 4720  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (3)...(2129)  
NAME/KEY: misc\_feature  
LOCATION: (1)...(4720)  
OTHER INFORMATION: n = A,T,C or G  
US-09-631-534-9

Alignment Scores:  
Pred. No.: 1,19e-253 Length: 4720  
Score: 3851.00 Matches: 699  
Percent Similarity: 99.71% Conservative: 0  
Best Local Similarity: 99.71% Mismatches: 2  
Query Match: 84.58% Indels: 0  
DB: Gaps: 0

US-09-634-252a-4 (1-832) x US-09-631-534-9 (1-4720)

OY 132 LeuAspThrLysAlaArgHisGlnGlnLysHisAsnLysAlaValHisLeuAlaGlnAla 151  
DB 27 CTTGACACAAAGGCAAGACACAGCAAAACATATATAGGCTGTCCATCTGGCCAGGCA 86  
OY 152 SerPheGlnIleGlnAlaPheGlySerLysPheIleLeuAspLeuIleLeuAsnAsnGly 171  
DB 87 AGCTTCAGATTGAAGGCTTGCGCTCCAAATTCCTTGTACCTCATACGAAACATGGT 146  
OY 172 LeuLeuSerSerAspTyrValGluIleHisTyrGlnAsnGlyLysProGlnTyrSerLys 191  
DB 147 TTGTGTCTCTGTATGTATGTGAGATTCTACACGAAATGGGAAACCACTACTCTAG 206  
OY 192 GlyGlyLysHisCysTyrTyrHisGlySerIleArgGlyValLysAspSerLysValAla 211  
DB 207 GGTGGAAGGCACTTACTACATGGAAGCATACAGAGGCTCCAAAGATCCAGGTGGCT 266  
OY 212 LeuSerThrCysAsnGlyLeuHisGlyMetPheGlnAspAspThrPheValTyrMetIle 231  
DB 267 CTGTCAACCTCATGACCTTCATGGGCATGTTGAAGATGATACCTGCTGTATATGATA 326  
OY 232 GluProLeuGlnLeuValHisAspGlyLysSerThrArgProHisIleIleGlnLys 251  
DB 327 GAGCCACTAGAGCTGTCTCATGTATGAGAAAGACAGGTCGACCAATATATCCAGAA 386  
OY 252 ThrLeuAlaGlyGlnTyrSerLysGlnMetLysAsnLeuThrMetGlnArgGlyAspGln 271  
DB 387 ACCTTGGAGGACAGATATTTAAGCAATGAGAAATCTCATGTATGAAAGAGGTGACAG 446  
OY 272 TrpProPheLeuSerGlnLeuGlnTyrLeuLysArgArgLysArgAlaValAsnProSer 291  
DB 447 TGGCCCTTCTCTCGAATTACAGTGTGAAAGAAAGAGACAGACAGTGAATCCATCA 506  
OY 292 ArgGlyIlePheGlnGlnMetLysTyrLeuGlnLeuMetIleValAsnAspHisLysThr 311  
DB 507 CGTGAATATTTGAAGAAATGAAATTTTGAACCTATGATTCGTAATGATCCAAACG 566  
OY 312 TyrLysLysHisArgSerSerHisAlaHisThrAsnAspPheAlaLysSerValValAsn 331  
DB 567 TATTAAGACATCGCTCTCTCTCATGACATACCAACAACCTTGCAAAAGTCCGTGTCAC 626  
OY 332 LeuValAspSerIleTyrLysGlnGlnLeuAsnThrArgValValLeuValAlaValGlu 351  
DB 627 CTGTGGATTTCTATTACAAGGAGAGCTCCACACCGAGGTGTCTGCTGGGTGATGAG 686  
OY 352 ThrTTrpThrGlnLysAspGlnIleAspIleThrThrAsnProValGlnMetLeuHisGlu 371  
DB 687 ACCTGGACTAGAGGATCAGATTGACATACCCCAACCTGTGGCATGTCTCCAGAG 746  
OY 372 PheSerLysTyrArgGlnArgGlnIleLysGlnHisAlaAspAlaValHisLeuIleSerArg 391  
DB 747 TTCTCAAAATACCGGACGACGATTAAGAGAGCATGCTGTGACACCTCATCTCGCGG 806

OY 392 ValThrPheHisTyrLysArgSerSerLeuSerTyrPheGlyGlyValCysSerArgThr 411  
DB 807 GTGACATTTCTACTATTAAGAAACCACTGTGAGTTACTTTGAAGGTGTCTGTCTCCACA 866  
OY 412 ArgGlyValAlaValAsnGlnTyrGlyLeuProMetAlaValAlaGlnValLeuSerGln 431  
DB 867 AGAGAGATTGGTGTGATGATGATGTGTCTTCCAAATGGCAATGGCAACAGATATATCCAG 926  
OY 432 SerLeuAlaGlnAsnLeuGlyIleGlnTyrGlnProSerSerArgLysProLysCysAsp 451  
DB 927 AGCCTGCTCAAAACCTTGAATCCAAATGGGAACCTTCTAGCAGAAACCAAAATGTGAC 986  
OY 452 CysThrGlnSerTrpGlyGlyCysIleMetGlnGlnTyrGlyValSerHisSerArgLys 471  
DB 987 TGCACAGAAATCCTGGGTGGCTGCATCATGAGGAAACAGGGGTCTCCATTCTCCGAAA 1046  
OY 472 PheSerLysCysSerIleLeuGlnTyrArgAspPheLeuGlnArgGlyGlyValCys 491  
DB 1047 TTTTCAAAAGTGACACATTTGGAGTATAGAGACTTTTACAGAGAGAGGTGGACCTGC 1106  
OY 492 LeuPheAsnArgProThrLysLeuPheGlnProThrGlnCysGlyAsnGlyTyrValGlu 511  
DB 1107 CTTTTCAAACAGCCACAAACGCTATTGAGCCACAGAAATGGAAATGGATACGTGGA 1166  
OY 512 AlaGlyGlnGlnCysAspCysGlyPheHisValGlnCysTyrGlyLeuCysCysLysLys 531  
DB 1167 GCTGGGAGAGAGTGTGATGTGTGTTCATGTGGAATCTATGGAATTTGTCTGTAGAGAA 1226  
OY 532 CysSerLeuSerAsnGlyValHisCysSerAspGlyProCysCysAsnAsnThrSerCys 551  
DB 1227 TGTTCCTCTCTCCAAAGGGGCTCAGTCAGAGCGAGGCTGCTGTACAAATCTCATGT 1286  
OY 552 LeuPheGlnProArgGlyTyrGlnCysArgAspAlaValAsnGlnCysAspIleThrGlu 571  
DB 1287 CTTTTCACCCACGAGAGGATGAATGCGGAGTGTGAACAGAGTGTGATTTACTGAA 1346  
OY 572 TyrCysThrGlyAspSerGlyLysCysProProAsnLeuHisLysGlnAspGlyTyrAla 591  
DB 1347 TATTGTACTGAGAGCTGTGTGATGCCCAAACTTTCATTAAGCAAGACGATATGCA 1406  
OY 592 CysAsnGlnAsnGlnGlyArgCysTyrAsnGlyGlnCysLysThrArgAspAsnGlnCys 611  
DB 1407 TGCAAATCAAAATCAGGGCGCTGCTCATGATGGCAATGGCAAGCCAGACACACAGTGT 1466  
OY 612 GlnTyrIleTrpLysThrLysAlaAlaGlySerAspLysPheCysTyrGlnLysLeuAsn 631  
DB 1467 CAGTACATCTGGGGACAAAGAGCTGCAGGGTGCAGAAAGTTCTGTATGAAAGCTGAAT 1526  
OY 632 ThrGlnGlyThrGlnLysGlyAsnGlyLysAspGlyAspArgTrpIleGlnCysSer 651  
DB 1527 ACAGAGGCGCACTGAGAGGGAACCTGCGGAGAGATGAGACCGGTGATTCAGTGCAGC 1586  
OY 652 LysHisAspValPheCysGlyPheLeuLeuCysThrAsnLeuThrArgAlaProArgIle 671  
DB 1587 AAACATGATGTGTCTGTGATTTCTACTGTATCCAAATCTTACTCAGGTCCACGTAT 1646  
OY 672 GlyGlnLeuGlnGlnIleIleProThrSerPheTyrHisGlnGlyArgValIleAsp 691  
DB 1647 GGTCAACTCCAGGATGATTCACAACTTCTTACCACTTCAAGGCGGGGTATTTGAC 1706  
OY 692 CysSerGlyAlaHisValValLeuAspAspAspThrAspValGlyTyrValAlaAspGly 711  
DB 1707 TGCAGTGTGTCCATGTATGTTTATGATGATATATACGATGTGGGCTATGAGAGATGA 1766  
OY 712 ThrProCysGlyProSerMetCysLeuAspArgLysCysLeuGlnIleGlnAlaLeu 731  
DB 1767 AGCCATGTGGCCGTCTATGATGTGTAGTCCGAGAGTGTCTCAAAATTCACACCCCTA 1826  
OY 732 AsnMetSerSerCysProLeuAspSerLysGlyLysValCysSerGlyHisGlyValCys 751  
DB 1827 AATATGACACAGCTGTCCACTCGATTCCAAAGGTAAGTCTGTGGGCGCATGGGTGTCT 1886

Oy	752	SeasnnglnualatrCy5IleCYAsnpPhehtrrtpmlaglyTtraspCy5SerTlearg	771
Dd	1887	AGTAATGACGACCACTTCGATTGTGATTTCACCTGGGCGAGGACAGATGCGATGTCCG	1946
Oy	772	AspProValAlrGaSnLeuHisProProLysAspLungLProLysGlyProSerAlatr	791
Dd	1947	GATCCAGATTAGGAACTTCACACCCGCCAAGGATAGAGACCAAGGCTTACGTGCCACC	2006
Oy	792	AsnLeuIleIleGlySerTleAlaGlyAlaIleLeuValAlaAlaIleValLeuGlyGly	811
Dd	2007	AATCTCAATTAATAGGCTCCATCGCTGTCGCCATCTGCTAGACAGCTATTGTCTTGGG3GC	2066
Oy	812	ThrLylTrpGlyPheLysAsnValLysArgArgPheAspProThrGlnGlnGlyPro	831
Dd	2067	ACAGGCTGGGATTTAAATAATGTCAAGAGAGAGGTTCCATCTACTACGACAGGCCACC	2126
Oy	832	Ile 832	
Dd	2127	ATC 2129	
RESULT 12			
US-10-260-506-9			
: Sequence 9, Application US/10260506			
: GENERAL INFORMATION:			
: APPLICANT: Shepard, Paul O.			
: APPLICANT: Baindur, Nand			
: APPLICANT: Deisher, Theresa A.			
: APPLICANT: Bishop, Paul D.			
: APPLICANT: Taft, David W.			
: TITLE OF INVENTION: DISINTEGRIN HOMOLOGUE, MAHBP			
: FILE REFERENCE: 98-2961			
: CURRENT APPLICATION NUMBER: US/10/260,506			
: CURRENT FILING DATE: 2002-09-27			
: PRIOR APPLICATION NUMBER: 60/092,371			
: PRIOR FILING DATE: 1998-07-10			
: PRIOR APPLICATION NUMBER: 60/147, 410			
: PRIOR FILING DATE: 1999-08-05			
: PRIOR APPLICATION NUMBER: 09/351,414			
: PRIOR FILING DATE: 1999-07-09			
: NUMBER OF SEQ ID NOS: 15			
: SOFTWARE: FastSeq for Windows Version 3.0			
: SEQ ID NO 9			
: LENGTH: 4720			
: TYPE: DNA			
: ORGANISM: Homo sapiens			
: FEATURE:			
: NAME/KEY: CDS			
: LOCATION: (3)...(2129)			
: FEATURE:			
: NAME/KEY: misc_feature			
: LOCATION: (1)...(4720)			
: OTHER INFORMATION: n = A,T,C or G			
US-10-260-506-9			
Alignment Scores:			
Pred. No.: 1,19e-253 Length: 4720			
Score: 3851.00 Matches: 699			
Percent Similarity: 99.71% Conservative: 0			
Best local Similarity: 99.71% Mismatches: 2			
Query Match: 84.58% Indels: 0			
DB: 43 Gaps: 0			
US-09-634-252A-4 (1-832) x US-10-260-506-9 (1-4720)			
Oy	132	LeuAspHrLysAlaArgHisGlnGlnLysHisAsnLysAlaValHisLeuAlaGlnAla	151
Dd	27	CTTACACAAAGGCAACACACACCAAAACATATATAGGCTGTCCATCTGGCCACAGCA	86
Oy	152	SerPheGlnIleGlnAlaPheGlySerLysPheIleLeuAspLeuIleLeuAsnGly	171
Dd	87	AGCTTCAGATGGAAGGCTTCGCTCCAAATTCATTCTTGACCTCATCTGACATGCAATGCT	346
Oy	172	LeuLeuSerSerAspTyValGlnIleHisTyGlnAsnGlyLysProGlnTySerLys	391

Dd	147	TTGTGTCTCTCGATTATCTGGAGATTCACTACGAATAATGGGAACACAGTAACTTAAG	206
Qy	192	GIYGLYGLNHISCYSTYTYRHHISGLYSERILEARGIYVALYASPSERYVALAIA	211
Dd	207	GGTGAGAGACACTGTTACTACCATGGAACATCAGAGCGCTCAAAAGCTCAAGGTGCT	266
Qy	212	LeuSerThrCysAsnGlyLeuHISGLYMeCPheGluAspAspThrPheValTYRMeLIE	231
Dd	267	CTGTCAACCTGCAATGGACTTCATGATGCAATGTTGAAGATGATGACTTCGTTATATGATA	326
Qy	232	GIUPROLEGIuLeuValHISASPGIuLYSSErThGIYARPROHISLIELEGILYs	251
Dd	327	GAGCCACATAGACCTGGTTCATATGAGAAAGCAGCGGTGACACATATAAATCCAGAAA	386
Qy	252	ThrLeuAlaGLIuGINTYrSerLYSGImeCLYsAsnLeuThrMeTGluARGIYASPGIn	271
Dd	387	ACCTTGCGCAGCAAGTATTCTAAGCAATAAGAAATCTCACTATGGAAAGAGGTGACAG	446
Qy	272	TrpProPheLeuSerGIuLeuGIuINTPrLeuLYsARGIuLYsARGIuValAsnProSer	291
Dd	447	TGGCCCTTCTCTCGAATTACAGTGGTGTGAAGAAGGAAGAGACAGTGAATTCATCA	506
Qy	292	ARGGIYIIErPheGLIuMeCLYsTYrLeuGIuLeuMeTLIEValIAsnAspHISLYsThr	311
Dd	507	CGTGGTATAATTTGAGAAATGAAATTTTGGAACTTATGTTGGTATGATCATCAAAAACG	566
Qy	312	TYrLYsLYSHISARGSerSerHISAlaHISThAsnAsnPheAlaLYsSerValIAsn	331
Dd	567	TATAGAAGACATCGCTCTTCTCATGCACTACCAACACTTTGCCAAAGTCCGTGGTCAAC	626
Qy	332	LeuValAspSerILETYrLYSGIuGLIuLeuAsnThrArgValIAlaValAlaGLIu	351
Dd	627	CTTGTGGATTCTATATTACAAAGAGCGCTCAACACACAGGGTGTCTCGTGGCGTARGAG	686
Qy	352	ThrTrpThrGluLYsAspSINTIleAspRIEThrThAsnProValGImeTLIEuHISGLIu	371
Dd	687	ACCTGGACGAGAAAGAGATCAGATGTCATCCACCACACCCCTGTGGAGATGCTCCATGAG	746
Qy	372	PheSerLYSTYrARGIuIARGIuLeuLYSGIuHISAlaAspAlaValHISLeuIIESerARG	391
Dd	747	TTCTCAAAATACCGCGCAGGCATTAAGCAGCACTGATGCTGTGCACCTCATCTGCGCG	806
Qy	392	ValIThrPheHISTYrLYsARGSerSerLeuSerTYrPheGLIYValCYsSerARGThr	411
Dd	807	GTGACATTTCACTATAGAGAAAGCACTGTGAGTTACTTTGAAGGTGTCTGTCTCGGACA	866
Qy	412	ARGGIYValGLYValAsnGIuTYrGIuLeuProMeAlaValAlaGLIuValLeuSerGIu	431
Dd	867	AGAGAGATGGTGTGATAGATGCTCTTCCAAATGGCAGCAAGATTAATATGCGAG	926
Qy	432	SerLeuAlaGLIuAsnLeuGLIuLEGINTPrGIuProSerSerLYsProLYsCYsASP	451
Dd	927	AGCTTGCGCTCAAAACCTTGTGAATTCATATGGAACTTTCTAGCGAAAGCCAAATGTGAC	986
Qy	452	CysThrGLIuSerTrpGLIYGLYCYsIIEmeTGluGIuThrGIuValSerHISerARGLYs	471
Dd	987	TGCACAGATCCTGGGGGTGGTGCATCANTGGAAGGAANAAGGGGTGTCCATTCTCGAAA	1046
Qy	472	PheSerLYsCYsSerIIEleuGLIuTYrARGAspPheLeuGLIuARGIYGLIYValCYs	491
Dd	1047	TTTTTCAAAAGTGCAGCATTTTGGAGATAGAGACTTTTTCACAGAGAGAGTGCAGCGCTGC	1107
Qy	492	LeuPheAsnARGProThrLYsLeuPheGIuProThrGIuCYsGLIYAsnGLIYTYrValGIu	511
Dd	1107	CTTTTTCACAGCGCCAAACAAGCTATTTTGAGCCCGACCGAAATGTGGAAATGATACGTGGAA	1166
Qy	512	AlaGLIYGLIuGLIuCYsAPCYsGLYrPheHISValIGLIuCYsTYrGLIuCYsCYsLYsLYs	531
Dd	1167	GCTGGGAGAGAGTGTGATGTGTGTTTCATGTGGAAATGCTATGATGATTTATGTCTAAGAAA	1222
Qy	532	CysSerLeuSerAsnGIuValHISCYsSerAspGIuProCYsCYsAsnThrSerCYs	551

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Db      1227 TGTCCCTTCACAGGGGGCTCACTGCAGCAGCGGGCCCTGCTGTAACATACCTCATGT 1286
OY      552 LeupheglnProArgglyTyrgluCysArgAspAlaValAsnGluCysAspIleThrGlu 571
      |||||||
Db      1287 CTTTTTCAGCCACGAGGATGAAATGCCGGATGCTGTAACGAGGTGATATTACTGAA 1346
OY      572 TyrcysThrGlyAspSerGlyGlnCysProProAsnLeuHisLysGlnAspGlyTyraAla 591
      |||||||
Db      1347 TATTGTACTGAGACTGTGGTACAGTGCCCAACAAATCTTCATAGCAGACGATATGCA 1406
OY      592 CysAsnGlnAsnGlnGlyArgCysTyraAsnGlyGluCysLysThrArgAspAsnGlnCys 611
      |||||||
Db      1407 TGCATTCAAATCAGGCGCGCTGCTACATGGCGAGTGCAGACGACAGACACAGTGT 1466
OY      612 GlnTyrlIeTrpGlyThrLysAlaAlaGlySerAspLysPheCysTyrgluLysLeuAsn 631
      |||||||
Db      1467 CAGTACATCTGGGGAACAAGGCTGCGAGGCTGACACAAGTTCTGCTATGAAAGCTGAAT 1526
OY      632 ThrGluGlyThrGluLysGlyAsnCysGlyLysAspGlyAspArgTrpIleGlnCysSer 651
      |||||||
Db      1527 ACAGAGGCACTGAGAGAGGAAGAACTCGGGAGAGATGAGACCGGTGATTCAGTCCAGC 1586
OY      652 LysHisAspValPheCysGlyPheLeuLeuCysThrAsnLeuThrArgAlaProArgIle 671
      |||||||
Db      1587 AAACATGATGTGTCTGTGGATCTTACTGTACCAATCTTACTCGAGCTCCAGTATT 1646
OY      672 GlyGlnLeuGlnGlyGluIleIleProThrSerPheTyrlHisGlnGlyArgValIleAsp 691
      |||||||
Db      1647 GGTCAACTTCAGGGTGATGATTCACAACTTCCTTACCATCAAGCCGGGTGATTGAC 1706
OY      692 CysSerGlyAlaHisValLeuAspAspAspThrAspValGlyTyraGluAspGly 711
      |||||||
Db      1707 TGCAGTGTGCCCATGTAGTTTAGATGATGATACGATCTGGGCTATGTAGAAAGATGA 1766
OY      712 ThrProCysGlyProSerMetMetCysLeuAspArgLysCysLeuGlnIleGlnAlaLeu 731
      |||||||
Db      1767 ACGCATGTGGCCCGCTGTATGATGTGTAGATCGAGTGTGCGCTATGTAGAAAGATGA 1826
OY      732 AsnMetSerSerCysProLeuAspSerLysGlyLysValCysSerGlyHisGlyValCys 751
      |||||||
Db      1827 AATATGAGCACTGTCCACTCGATTCCAAAGGTAAGTCTGTTCGGCCATGGGCTGTGT 1886
OY      752 SerAsnGluAlaThrCysIleCysAspPheThrTrpAlaGlyThrAspCysSerIleArg 771
      |||||||
Db      1887 AGTAATGAGCCACCTGCAATTTGTGATTTACCTGGCGAGGACAGATTGCAGTATCCGG 1946
OY      772 AsproValArgAsnLeuHisProProLysAspGluGlyProLysGlyProSerAlaThr 791
      |||||||
Db      1947 GATCCAGTTAGAACCTTCACCCCCCAAGGATGAAGAGACCAAGGCTCTAGTGCACC 2006
OY      792 AsnLeuIleIleGlySerIleAlaGlyAlaIleLeuValAlaAlaIleValLeuGlyGly 811
      |||||||
Db      2007 AATTCATATATAGGCTCCATCGCTGTGTCATCTGTAGCAGCTATTGTCTTG6GGGC 2066
OY      812 ThrGlyTrpGlyPheLysAsnValLysLysArgArgPheAspProThrGlnGlnGlyPro 831
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Db      2067 ACAGGCTGGGATTAAATGCAAGAGAGAGGTTGATCTTACTCAGCAAGGCCCC 2126
OY      832 Ile 832
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Db      2127 ATC 2129
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Search completed: June 1, 2003, 20:13:49  
Job time : 4610 secs





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Qy 761 PheHrTPAlaGlyThrAspCysSerIleArgAspProValArgAsnLeuHisPropo 780  
Db 2350 TTCACTGGGAGGAGACGATTGCGATATCCGGATCCAGTATAGAACCTTACCCCCC 2409  
Qy 781 LysAspGlyGlyProLysGlyProSerAlaThrAsnLeuIleIleGlySerIleAlaGly 800  
Db 2410 AAGATGAAGGAGCCCAAGGCTCTAGTGCACCAATCTCATTAATAGGCTCATCGCTGCT 2469  
Qy 801 AlalleuValAlaAlaIleValleuGlyGlyThrGlyTyrGlyPheLysAsnValLys 820  
Db 2470 GCCATCCGAGGAGCGCTATTGTCTTGGGGGACAGGCTGGGATTTAAAAATGTCAG 2529  
Qy 821 LysArgArgPheAspProThrGlnGlnGlyProIle 832  
Db 2530 AAGAGAAGCTTCGATCTACTACAGCAAGGCCCATC 2565  
RESULT 2  
US-10-126-052A-149  
Sequence 149, Application US/10126052A  
GENERAL INFORMATION:  
APPLICANT: Mutray, Richard  
APPLICANT: Aziz, Natasha  
APPLICANT: Eos Biotechnology, Inc.  
TITLE OF INVENTION: Methods of Diagnosis of Lung Cancer, Compositions and  
TITLE OF INVENTION: Methods of Screening for Modulators of Lung Cancer  
FILE REFERENCE: 018501-001530US  
CURRENT APPLICATION NUMBER: US/10/126,052A  
CURRENT FILING DATE: 2002-04-18  
PRIOR APPLICATION NUMBER: US 60/284,770  
PRIOR FILING DATE: 2001-04-18  
PRIOR APPLICATION NUMBER: US 60/290,492  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: US 60/339,245  
PRIOR FILING DATE: 2001-11-09  
PRIOR APPLICATION NUMBER: US 60/350,666  
PRIOR FILING DATE: 2001-11-13  
PRIOR APPLICATION NUMBER: US 60/334,370  
PRIOR FILING DATE: 2001-11-29  
PRIOR APPLICATION NUMBER: US 60/372,246  
PRIOR FILING DATE: 2002-04-12  
NUMBER OF SEQ ID NOS: 691  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 149  
LENGTH: 3054  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-126-052A-149  
Alignment Scores:  
Pred. No.: 0 Length: 3054  
Score: 4553.00 Matches: 832  
Percent Similarity: 100.008 Conservative: 0  
Best Local Similarity: 100.008 Mismatches: 0  
Query Match: 100.008 Indels: 0  
DB: 9 Gaps: 0  
US-09-634-252A-4 (1-832) x US-10-126-052A-149 (1-3054)  
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Db 224 ATGAGAGCGCGCGGAGAGCTCGCGGAGCGCGCGCTGGCGGCTGCAGCTTCGCGC 283  
Qy 21 AlasecysGlyProGlnArgGlyProAlaGlySerValProAlaSerAlaProAlaArg 40  
Db 284 GCTTCCTGGGCGCCCAAGGCGGCGCGCGCTGGGCTGCAGCGCCCGCGCGCGC 343  
Qy 41 ThrProGlyArgLeuLeuValLeuLeuLeuLeuProProLeuAlaAlaSerSer 60  
Db 344 ACGCGCGCGCGCGCGCTTCCTTCCTTCGCGCGCGCGCTGCAGCGCGCGCGCTTC 403  
Qy 61 ArgProArgAlaTyrGlyAlaAlaAlaProSerAlaProHisTyrAsnGlyThrAlaGlu 80

Db 404 CGGCCCCGGCGCGGGGGGCTGCTGCGCCAGCGCTCCGATTCGAATGAATGACAGAA 463  
Qy 81 LysAsnLeuGlyValLeuAlaAspGluAspAspThrLeuGlnGlnAsnSerSerAsn 100  
Db 464 AAAAATTTGGAGTCTCGCGAGATGAAGACAAATTCATTCAGACAGATACAGAGTAAT 523  
Qy 101 IleSerTyrSerAsnAlaMetGlnLysGluIleThrLeuProSerArgLeuIleTyrTyr 120  
Db 524 ATCAGTTACAGCATGCATGCAGAAAGAAATCAGACCTGCTTCAGACCTCATATATTAC 583  
Qy 121 IleAsnGlnAspSerGluSerProTyrHisValLeuAspThrLysAlaArgHisGln 140  
Db 584 ATCAACCAAGACCTCGAAAGCCCTTATCAGCTTCTTGACACAAAGGACAGACACAGCAA 643  
Qy 141 LysHisAsnLysAlaValHisLeuAlaGlnAlaSerPheGlnIleGluAlaPheGlySer 160  
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Qy 201 SerIleArgGlyValLysAspSerLysValAlaLeuSerThrCysAsnGlyLeuHisGly 220  
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Qy 241 LysSerThrGlyArgProHisIleIleGlnLysThrLeuAlaGlyGlnTyrSerLysGln 260  
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Qy 261 MelLysAsnLeuThrMetGluArgGlyAspGlnTyrProPheLeuSerGluLeuGlnTyr 280  
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Qy 301 LeuGluLeuMetIleValAsnAspHisLysThrTyrLysLysHisArgSerHisAla 320  
Db 1124 TTGGAATCTATGATGTATGATATGATCAAAAGCATATAGAAAGCATGCTTCTCATGCA 1183  
Qy 321 HisThrAsnAspPheAlaLysSerValValAsnLeuValAspSerIleTyrLysGluGln 340  
Db 1184 CATACCAACAACCTTTCAAAGTCCGTCGTCACCTGTGATTCATTTCAAGAGACAG 1243  
Qy 341 LeuAsnThrArgValValLeuValAlaValGluThrTyrPheGluLysAspGlnIleAsp 360  
Db 1244 CTCACACCAAGGTTGCTGCTGCTGCTGCTGAGAACCTGGACCTAGAAAGATTCAGATTGAC 1303  
Qy 361 IleThrThrAsnProValGlnMetLeuHisGluPheSerLysTyrArgGlnArgIleLys 380  
Db 1304 ATCACCACCAACCCCTGCGAGATGCTCATGATGCTTCAAAATACCGCGACCATTAAG 1363  
Qy 381 GlnHisAlaAspAlaValHisLeuIleSerArgValThrPheHisTyrLysArgSerSer 400  
Db 1364 CAGCATGCTGATGCTGTGACCTCATCTCCGGGTGACATTTACATTAAGAAAGACAGT 1423  
Qy 401 LeuSerTyrPheGlyGlyValCysSerArgThrArgGlyValGlyAlaAsnGlyTyrGly 420  
Db 1424 CTCAGTTACTTGGAGAGTGTCTTCTTCGACAAAGAGAGATTGCTGGAATGAGTATGCT 1483  
Qy 421 LeuProMetAlaValAlaGlnValLeuSerGlnSerLeuAlaGlnAsnLeuGlyIleGln 440



1484 CTTCCAAATGGCAGTGGCACAACTATTATCGAGAGCTGGCTCAAAACCTTGGAAATCCAA 1543  
OY 441 TTPGluProSerSerArgLysProLysCysAspCysThrGluSerTrpGlyLysCysIle 460  
DB 1544 TGGGAACCTTCTAGCAGAAAGCAAAATGTGACTGCACAGATCTCTGGGCTGGCTGCATC 1603  
OY 461 MetGluGluThrGlyValSerHisSerArgLysPheSerLysCysSerIleLeuGluLys 480  
DB 1604 ATGGAGAGAAACAGGGGTGTCCATTCTCGAAAATTTTCAAAATGTGACAGCAATTTTGGAGTAT 1663  
OY 481 ArgAspPheLeuGluArgLysGlyValCysLeuPheAsnArgProThrLysLeuPhe 500  
DB 1664 AAGAGACTTTTACAGAGAGAGAGAGTGGAGCTGCTTTTAAACAGGCCAACAACATATT 1723  
OY 501 GluProThrGluCysGlyAsnGlyTyrrValGluAlaGlyLysCysAspCysGlyPhe 520  
DB 1724 GAGCCACCGAATGTGGAAATGGATACGTGGAAGCTGGGAGAGAGAGTGTATGTGGTATT 1783  
OY 521 HisValGluCysTyrrGlyLeuGlyCysLysLysCysSerLeuSerAsnGlyAlaHisCys 540  
DB 1784 CATGTGGAAATGCTATGGATTATGCTGTAAAGAAATGTTCCCTCCACAGGGGCTCCTGC 1843  
OY 541 SerAspGlyProCysCysAsnAsnThrSerCysLeuPheGluProArgGlyTyrrGlyCys 560  
DB 1844 ACGGAGGGGCTCGCTGTAACAATACCTCATGCTTTTACAGCCACGAGGATATGATGC 1903  
OY 561 ArgAspAlaValAsnGluCysAspIleThrGlyTyrrCysThrGlyAspSerGlyLysCys 580  
DB 1904 CCGGAGTGTGTGAAACAGTGTATATTACTGAATATTGTACTGGAACACTGTGCTCAGTGC 1963  
OY 581 ProProAsnLeuHisLysGlnAspGlyTyrrValCysAsnGluAsnGlnGlyArgCysTyrr 600  
DB 1964 CCACCAATCTTCTATAGCAAGACGATATGCTGCAATCAAAATATAGGGGCTCCTCTAC 2023  
OY 601 AsnGlyGluCysLysThrArgAspAsnGlnCysGlnTyrrIleTrpGlyThrLysAlaIle 620  
DB 2024 AATGCGAGTGTGCAAGACCAAGACCAACCAAGTGTCACTACATCTGGGGAACAAAGCTGCA 2083  
OY 621 GlySerAspLysPheCysTyrrGlyLysLeuAsnThrGluGlyThrGluLysGlyAsnGly 640  
DB 2084 GGGTCTGACAAAGTCTGCTATGAAAGCTGAATATACGAAGGCACTAGAGAGGAAACTGC 2143  
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OY 661 LeuCysThrAsnLeuThrArgAlaProArgIleGlyGlnLeuGlnGlyIleIlePro 680  
DB 2204 CTCTGTACCAATCTTACTGAGCTCCACGATTTGTCACCTTCAGGGGTGAGATCATTC 2263  
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DB 2264 ACTTCTCTTACCATTAAGCGCGGTGATTTGACTGCAGTGTGCCCATGTAGTTTATGAT 2323  
OY 701 AspAspThrAspValGlyTyrrValGluAspGlyThrProCysGlyProSerMetMetCys 720  
DB 2324 GATGATACGATGTGGCTATGTAGAAAGATGAAGACGATGTGGCCGTCTATGATGATGT 2383  
OY 721 LeuAspArgLysCysLeuGlnIleGlnAlaLeuAsnMetSerSerCysProLeuAspSer 740  
DB 2384 TTGAGATCGGAAGTGTCTACAAATTTCAAGCCCTAAATATGAGCAGCTGTCCACGATGCC 2443  
OY 741 LysGlyLysValCysSerGlyHisGlyValCysSerAsnGluAlaThrCysIleCysAsp 760  
DB 2444 AAGGTAATATCTGTTGGGCGCATGGGCTGTAGTATAGAACCAACCTGCATTTTGAT 2503  
OY 761 PheThrTrpAlaGlyThrAspCysSerIleArgAspProValArgAsnLeuHisProPro 780  
DB 2504 TTACACCTGGGCGAGAGATTCAGATTCGGGATTCACCTTAGGAACCTTACCCCCC 2563  
OY 781 LysAspGluGlyProLysGlyProSerAlaThrAsnLeuIleIleGlySerIleAlaGly 800  
DB 2564 AAGGATAAAGACCAAGGCTCTAGTCCACCAATCTCATATAGGCTCATCGCTGCT 2623

OY 801 AlaIleLeuValAlaAlaIleValLeuGlyLysThrGlyTrpGlyPheLysAsnValLys 820  
DB 2624 GCCATCTCGTGTAGCAGTATGTTGCTTGGGGCACAGGCTGGGATTTAAAAATGTCAAG 2683  
OY 821 LysArgArgPheAspProThrGlnGlnGlyProIle 832  
DB 2684 AAGAGAGGTTGATCTTACTACTACGACAGGCCCATC 2719  
RESULT 3  
US-10-126-052A-324  
Sequence 324, Application US/10126052A  
GENERAL INFORMATION:  
APPLICANT: Aziz, Natasha  
APPLICANT: Murray, Richard  
TITLE OF INVENTION: Methods of diagnosis of Lung Cancer, Compositions and  
TITLE OF INVENTION: Methods of Screening for Modulators of Lung Cancer  
FILE REFERENCE: 018501-001530US  
CURRENT APPLICATION NUMBER: US/10/126, 052A  
CURRENT FILING DATE: 2002-04-18  
PRIOR APPLICATION NUMBER: US 60/284, 770  
PRIOR FILING DATE: 2001-04-18  
PRIOR APPLICATION NUMBER: US 60/290, 492  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: US 60/339, 245  
PRIOR FILING DATE: 2001-11-09  
PRIOR APPLICATION NUMBER: US 60/350, 666  
PRIOR FILING DATE: 2001-11-13  
PRIOR APPLICATION NUMBER: US 60/334, 370  
PRIOR FILING DATE: 2001-11-29  
PRIOR APPLICATION NUMBER: US 60/372, 246  
NUMBER OF SEQ ID NOS: 691  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 324  
LENGTH: 3054  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-126-052A-324  
US-10-126-052A-324 (1-832) x US-10-126-052A-324 (1-3054)  
Alignment Scores:  
Pred. No.: 0 Length: 3054  
Score: 4553.00 Matches: 832  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Gaps: 0  
DB: 9  
OY 1 MetLysProProGlySerSerArgGlnProProLeuAlaGlyCysSerLeuAlaGly 20  
DB 224 ATGAGCGCGCGCGCGAGCTGCGCGAGCCGCTGGCGGCTGCGAGCTTGGCGGC 283  
OY 21 AlaSerCysGlyProGlnArgGlyProAlaGlySerValProAlaSerAlaProAlaArg 40  
DB 284 GCTTCTGCGGCGCCCAAGCGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 343  
OY 41 ThrProProCysArgLeuLeuValLeuLeuLeuProProLeuAlaIleSer 60  
DB 344 ACGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 403  
OY 61 ArgProArgAlaTrpGlyAlaAlaAlaProSerAlaProHisTrpAsnGluThrAlaGlu 80  
DB 404 CGGCGCGCGCGCGCGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 463  
OY 81 LysAsnLeuGlyValLeuAlaAspGluAspAsnThrLeuGlnGlnAsnSerSerAsn 100  
DB 464 AAAAATTTGGAGATCTCTGCGCAGATGAAGACAAATATTCGAACAGATAGCAGCAGTAAT 523  
OY 101 IleSerTyrSerAsnAlaMetGlnLysGluIleThrLeuProSerArgLeuIleTyrTyr 120



Db 524 ATCAGTTACGCAATGCAATGCAAGAAATCACACTGCTTCAGACTCATATATTTAC 583  
OY 121 ILeasnGlnAspSerGlnSerProTyrHisValIleuAspThrLysAlaArgHisGln 140  
Db 584 ATCAACCAAGACTCGAAAGCCCTTATTCAGCTTTCGACCAAGGACAGACACCAACAA 643  
OY 141 LysHisAsnLysAlaValHisIleuAlaGlnAlaSerPheGlnIleGluAlaPheGlySer 160  
Db 644 AAACATATAATAGGCTGTCCATCTGGCCCAAGGCAAGCTTCAGATTGAGCTTCGAGTCC 703  
OY 161 LysPheIleIleuAspLeuIleuAsnAsnGlyIleuLeuSerSerSpTyValGluIle 180  
Db 704 AAATTCATTTCTTGACTCTGACTGAAACAATGGTTGTCTCTCATTAATATGGGAATTT 763  
OY 181 HsTyrGluAsnGlyLysProGlnTyrSerLysGlyGluHisGlyTyrTyrHisGly 200  
Db 764 CACTACGAAATGGGAACACAGTACTTAAGGGTGGAGAGACAGCTTACTACCAATGGA 823  
OY 201 SerIleArgGlyValLysAspSerLysValAlaLeuSerThrCysAsnGlyLeuHisGly 220  
Db 824 ACCATCAGAGGCGTCAAAAGACTCCAAAGTGGCTCTGTCAACCTGCAATGAGACTTCAAGGC 883  
OY 221 MetPheGluAspAspThrPheValTyrMetIleGluProLeuGluLeuValHisAspGlu 240  
Db 884 ATGTTTGAAGATGATACCTTCGTGATATGATAGACCCTAGAGCTGGTTCATGAGAGAG 943  
OY 241 LysSerThrGlyArgProHisIleIleGlnLysThrLeuAlaGlyGlnTyrSerLysGln 260  
Db 944 AAAGACAGCGTGCAGCACATATATCCAGAAACCTTGGCAGACAGTATTCATACAA 1003  
OY 261 MetLysAsnLeuThrMetGluArgGlyAspGlnTyrProPheLeuSerGluLeuGlnTyr 280  
Db 1004 ATGAGAATACTCACTATGCAAGAGCTGACACAGTGGCCCTTCTCTGCAATATACATGCG 1063  
OY 281 LeuLysArgArgLysArgAlaValAsnProSerArgGlyTyrLeuGluGluMetLysTyr 300  
Db 1064 TTGAAAAGAGAGAGAGACAGTGAATCCATCCAGTGTATATTTGAAGAAATATAT 1123  
OY 301 LeuGluLeuMetIleValAsnAspHisLysThrTyrLysLysHisArgSerHisAla 320  
Db 1124 TTGGAACCTATGATGTTTAAATGATCCAAACCTATAAGAGAGATGCTTCTTCATGCA 1183  
OY 321 HisThrAsnAspPheAlaLysSerValValAsnLeuValAspSerIleTyrLysGln 340  
Db 1184 CATACCAACACTTTGCCAAAGTCCGCGTCACCTGTGATCTTATTTCAAGAGAACAG 1243  
OY 341 LeuAsnThrArgValValLeuValAlaValGluThrTyrPheGluLysAspGlnIleAsp 360  
Db 1244 CTCACACCAAGGGTGTCTGCTGGCTGTAGAGACTGGACTGAGAAAGGATTCAGATTGAC 1303  
OY 361 IleThrThrAsnProValGlnMetLeuHisGluPheSerLysTyrArgGlnArgIleLys 380  
Db 1304 ATCACCAACCAACCTGTGCAGATGCTCATGAGTCTCAAAATACCGGCGCCCATTAAG 1363  
OY 381 GlnHisAlaAspAlaValHisIleuIleSerArgValThrPheHisTyrLysArgSerSer 400  
Db 1364 CAGCATGCTGATGCTGTGCACCTCATCTGCGGGTGACATTTCCATATAAGAACAGTAGT 1423  
OY 401 LeuSerTyrPheGlyGlyValLysSerArgThrArgGlyValGlyValAsnGluTyrGly 420  
Db 1424 CTGAGTACTTTGGAGAGTGTCTGTCTCCACACAGAGAGAGTGTGGTGAATGAGTAGGT 1483  
OY 421 LeuProMetAlaValAlaGlnValLeuSerGlnSerLeuAlaGlnAsnLeuGlyIleGln 440  
Db 1484 CTTCCCAATGGCAGTGCACCAAGATATTATCGCAGAGGCTGGCTCAAAACCTTGGAAATCCA 1543  
OY 441 TyrGluProSerSerArgLysProLysCysAspCysThrGluSerThrGlyGlyCysIle 460  
Db 1544 TGGGAACCTTTTACGCAAGAACCAAAATGTGACTGCACAGAAATCCGGGGTGGCTGCATC 1603  
OY 461 MetGluGluThrGlyValSerHisSerArgLysPheSerLysCysSerIleLeuGluTyr 480  
Db 1604 ATGGAGGAACAGGGGTGTCCCATTTCTCGAAATTTTCAAGTGCAGCATTTTGGAGTAT 1663

OY 481 ArgAspPheLeuGlnArgGlyGlyValAlaCysLeuPheAsnArgProThrLysLeuPhe 500  
Db 1664 AGAGACTTTTACAGAGAGAGGTGGAGCTGCTTTTCAACAGAGCCCAACAAAGCTATTT 1723  
OY 501 GluProThrGluCysGlyAsnGlyTyrValGluAlaGlyGluGluCysAspCysGlyPhe 520  
Db 1724 GAGCCACAGGAATGTGAAATGATAGCTGGAGAGCTGGGGAGAGTGTGATTTGGTTT 1783  
OY 521 HisValGluCysTyrGlyLeuCysCysLysLysCysSerLeuSerAsnGlyAlaHisCys 540  
Db 1784 CATGTGAAATGCTATGATTAATGCTGAAGAAATGTTCCCTCCAAAGGGGCTCACAGC 1843  
OY 541 SerAspGlyProCysCysAsnAsnThrSerCysLeuPheGlnProArgGlyTyrGluCys 560  
Db 1844 AGCAGAGGCGCCCTGCTGTACAAATACCTCATGCTTTTTCAGCCACAGAGGTATGAAATGC 1903  
OY 561 ArgAspAlaValAsnGluCysAspIleThrGluTyrCysThrGlyAspSerGlyGlnCys 580  
Db 1904 CCGGATCTGTGAACGAGTGTGATTAATCTGAATATTTCTACTGGAGACTGTGTCAGTGC 1963  
OY 581 ProProAsnLeuHisLysGlnAspGlyTyrAlaCysAsnGlnAsnGlnGlyArgCysTyr 600  
Db 1964 CCACCAATCTTCAATAAGCAAGACGATATGCAATGCAAAATCAAGGCGCTGCTTAC 2023  
OY 601 AsnGlyGluCysLysThrArgAspAsnGlnCysGlnTyrIleTyrGlyThrLysAlaAla 620  
Db 2024 AATGGCAGTGCAGACACAGACAGACAGTCTGATCATCTGGGACAAAGGCTGCA 2083  
OY 621 GlySerAspLysPheCysTyrGluLysLeuAsnThrGluGlyThrGlyLysGlyAsnCys 640  
Db 2084 GGGCTGTACAAGTCTCTCTATGAAGAACTGAAATACAGAGCAGCTGAGAAAGGAACTGC 2143  
OY 641 GlyLysAspGlyAspArgTyrPheGlnCysSerLysHisAspValPheCysGlyPheLeu 660  
Db 2144 GGGAGAGATGAGACCGGTGATTCAGTGCAGCAAACTGATGTGTCTGTGATTCCTTA 2203  
OY 661 LeuCysThrAsnLeuThrArgAlaProArgIleGlyGlnLeuGlnGlyGlnIleIlePro 680  
Db 2204 CTCTGTACCAATCTTACTCCAGCTCCACGTAATTTGTGTCACTTCAGGGGTGAGATTCCTCA 2263  
OY 681 ThrSerPheTyrHisGlnGlyArgValIleAspCysSerGlyAlaHisValIleuAsp 700  
Db 2264 ACTTCTCTTACCACTTCAAGGCGGGGTGATGACAGTGCAGTGTGCCATGTAGTTAGAT 2323  
OY 701 AspAspThrAspValGlyTyrValGluAspGlyThrProCysGlyProSerMetMetCys 720  
Db 2324 GATGATACGGATGTGGCTATGTAGAAAGATGGAAGCCCATGTGGCCGCTATATGATGTGT 2383  
OY 721 LeuAspArgLysCysLeuGlnIleGlnAlaLeuAsnMetSerSerCysProLeuAspSer 740  
Db 2384 TTGATATGGAAGTGCCTTAACAATTCAGGCTTAATATATGACACACTGTCCATGATTCC 2443  
OY 741 LysGlyLysValLysSerGlyHisGlyValLysSerAsnGluAlaThrCysIleCysAsp 760  
Db 2444 AAGGGTAAAGCTGTGGGGCATAGGGGTGTGTGATATGAAAGCACCTCGCATTTGTGAT 2503  
OY 761 PheThrTrpAlaGlyThrAspCysSerIleArgAspProValArgAsnLeuHisProPro 780  
Db 2504 TTCACTCGGCGAGGAGACAGATTGCAATGCCGATTCAGTTAGGAACCTTCACCCCCC 2563  
OY 781 LysAspGluGlyProLysGlyProSerAlaThrAsnLeuIleIleGlySerIleAlaGly 800  
Db 2564 AAGGATACAGAGACCAAGGGGCTCAGTGCACCAATCATTAATAGCTTCATGCTGCTGT 2623  
OY 801 AlaIleLeuValAlaAlaIleValLeuGlyGlyThrGlyThrGlyPheLysAsnValLys 820  
Db 2624 GCCATTCGTGAGCAGCTATTTCTTGGGGGCACAGCTCGGAGTTTAAAAAATGTCAG 2683  
OY 821 LysArgArgPheAspProThrGlnGlnGlyProIle 832  
Db 2684 AAGGAAAGTTCATCTTACTACAGCAAGGCCCATTC 2719







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Db      296 TCGACACACATATATATCCAGAAACCTTGGCAGACAGTATTCTAAGCAATGAAGATCTP 355
Qy      264 UTHRMETGLUARGGLYASPOLNTPRPPHLEUSERGLUENGLTRPLEUUSYASGAR 284
Db      356 CACTATGGAAGAGGTGACAGGAGGCTTCTCTCTGAAATTAAGGGTGTGAAGAAAG 415
Qy      284 GLYSARGALAAVALASPROSERARGLYLEPHEGLUGLUMELSTYRLEUGLUSAME 304
Db      416 GAAGAGAGCAGTGAATCCATCAGTGGTATATTGAAGAAATGAATATTGGACACTTAT 475
Qy      304 LILEVALASNASPHISLYSTHRTYRILYSLSYSHSARGSERSHISALHISTHRASNAS 324
Db      476 GATTGTTAATGATCACAAAACGTATAGAAGCATCGCTCTTCATCATCAGATCAACA 535
Qy      324 NPHEALALYSSESRVALVALASNULEVALASPSERTILETYRGLUGLNULEUSNTPRAR 344
Db      536 CTTTGGCAAAAGCTCGGTGCTCAACCTTGAGTCTATTATTAACAGGAGCGCTCAACA 595
Qy      344 GVALVALLEUVALALAVAILUTHTTPTHTGILULYSASPGILILEASPILETHTRAS 364
Db      596 GGTTCCTGCTGGTGGCTGAGAGACCTGGACTGAGAAGATCAGATTGCATCCACCA 655
Qy      364 NPROYALINMETLEUHSGLUPHESERTYRARGGLNARGILEYSGLINHISALAAS 384
Db      656 CCTGTGCAGATCTCCATGAGTCTCAAAAATACCGGACGCGATTAAGCAGCATGCTGA 715
Qy      384 PALAVALHISLEULESERARGVALTHRPHENISTYRILYSARGSERLEUSERTYRPH 404
Db      716 TGTGTGCACCTCATCTCCGGGGTGACATTTCTCACTATAGAAGAGCGCTGTGAGTACT 775
Qy      404 EGLYGLYVALCYSSERARGTHARGLYVALGLYVALASNUGLUTYRGLYLEUPROMETAL 424
Db      776 TGGAGGTGCTCTGTTCTCGCACAGAGAGAGTGGTGGAATGAGATGCTCTTCCAA 835
Qy      424 AVALALAGINVALLEUSERGLINSEULEUALAGINASNULEGLYILEGLINTRPGUPROSA 444
Db      836 AGTGGACAAAGTATTTTCGACAGACCTGTGCTCAAAACCTTGGAATCCAAAGGGAACCTTC 895
Qy      444 RSEARGLYSPROLYSCYSPSPCTSTHRLUSERTTPGLYGLYCYSITLLETGLUGLUT 464
Db      896 TACACAAAAGCCAAAATGTGACTGCACAGCAATCTTGCGGTGCTGCAATCGGAGAAC 955
Qy      464 RELYVALSERHISSEARGLYSPHESERTYSCYSERTILEUGLUTYRARGASPHELA 484
Db      956 AGGGGTGCTCCATTTCTCGAAAATTTTCAAAAGTGCAGATTTTGGAGTATAGAGACTTTT 1015
Qy      484 UGLINATGGLYGLYLYALACYSLEUPHEASNAARGPROTHRLYSLEUPHEGLUPROTHRGL 504
Db      1016 ACAGAGAGAGAGGTGGAGGCTGCTTTTCAACAGGCCCAAAACCTATTATGAGCCACAGGA 1075
Qy      504 UCYSGLYASNGLYTYRVALGLINULAGLYUGLUCYSASPCYSGLYPHEHISVALGLUCY 524
Db      1076 ATGTGAAAATGTGATACGTGGAACCTGGGAGAGGTGATGTGGTGTTCATGTGGGAAT 1135
Qy      524 STYRGLYLEUCYSCYLSLYSCYSSERLEUSEASNGLYALAHISCYSESRASPGLYPR 544
Db      1136 CTATGATATATGCTGTAAAGAAATGTTCCCTCCCAACGGGGCTACATGACGACGGGCC 1195
Qy      544 OCYSYCSASNAASNTHSERCYSLEUPHEGLINPROARGGLYTYRGLUCYSARGASPLAVALA 564
Db      1196 CTGCTGTAAACAATCACTCATGCTCTTTTTCAGCCACAGAGGTATGAAGCGGGGATGCTGT 1255
Qy      564 LANSGLUCYASASPILETHRGILUTYRYSSTHRLYASPSERGLGLUCYSPROPROFASNL 584
Db      1256 GAACGAGTGTGATATTACTGAATATTGTACTGAGACTCTGTCAGTCCAGCCACCAATCT 1315
Qy      584 UHISLYSGLINASPGLYTYRALACYSASNGINASNGINLYARGCYSTYRASNGLYLCUCY 604
Db      1316 TCATAAGCAAGAGAGGTATGATGCAATCAAAATCAGGGCGCTGCTACAAATGGCGAGTG 1375
Qy      604 SLYSTHRRARGASPARSGLINCYSGLINTYRIETTPGLYTHLYALALAEIYSERASPLY 624

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Db      1376 CAAGACCAGAGACCAACGAGTGTACATCTGGGGAAACAAAGCGCTGAGGCTGCACAA 1435
Qy      624 SPHECYSTYRGLULYSLEUASNTHRGLUTYTHGLULYSGLYASNCYSGLYLSASPGIL 644
Db      1436 GTTTCGTATGAAAAGCTGGAATACAGAGGACACTGAGAGGGAANAATCTCGGGAAGATGG 1495
Qy      644 YASPARGTTPILLEGINCYSSERLYSHISASPVALPHECYSGLYPHELEULEUCYSTHRAS 664
Db      1496 AGACGGGTGATTCAGTGCAGACCAAAACATGATGTGTTCTGTGGATTTCTTACCTGACCAA 1555
Qy      664 NLEUTHARGALAPROARGILEGLYGLINLEUGLNGLYLUILELLEPOTHRSERPHETY 684
Db      1556 TCTTACTGAGCTCCAGCTGATTTGCTCAACTTCAGAGGTGAGATCATTTCCAACTTCCCTTCTA 1615
Qy      684 RHISGLINGLYARGVALILEASPCYSSERGLYALAHISVALYALLEUSPASPARPTHRAS 704
Db      1616 CCATCAAGGCGGGGTGATGTACTGCAGAGTGAGGCCCATGTACTTATGATGATGATACCGGA 1675
Qy      704 PVALGLYTYRVALJLULASPGLYTHRPROCYSGLYPROSERMETECYSLASPARGLY 724
Db      1676 TGTGGCTATGTAGAAAGTGAAGAGCCATGTGGCCGCTGTGATGTGTTTAGATCGGAA 1735
Qy      724 SCYSLUENGLINLEGLNALAUEASNMETSERSECYSPROLEUASPSERTYSGLYLSVA 744
Db      1736 GTCCCTACAAATTCAAAGCCCTAAATATGAGCAGCGCTGTCCATCGATTCCAAAGGTTAAAGT 1795
Qy      744 ICYSSERGLYHISGLYVALCYSSERASNGLYALATHRCYSITLLECYASAPPHETHTRPA 764
Db      1796 CTGTTCCGGGCGCATGGGTGTGTAGTAAGAACCACTGCAATTTGTGTGATTCACCTGGGC 1855
Qy      764 AGLYTHASPCYSSERTILEARGASPROVALARGASNULEHISPPOPOLYASPGILUGL 784
Db      1856 AGGACAGATGTGACAGTATCCGGGATCCAGTTAGGAGACTTCCACCCCAAGAGATGAAGG 1915
Qy      784 YPROLYSGLYPROSERALATHRASNULEILEGLYSERTILEALAGLYALALEUVA 804
Db      1916 ACCCAAGGCTCTGATGCTCCACCAATCTCATATAGCGCTCCCTGCTGCTCATCTGCT 1975
Qy      804 LALAALILEVALLEUGLYGLYTHRGILYTRGILYPHELYSASNUALLYLSYASARGATRGPH 824
Db      1976 AGCAGCTATTGTCCTTGGGGGACACAGCTGGGGGATTTAAANAATGTCAAGAGAGAGGCTT 2035
Qy      824 EASPPROTHRGINGLINGLYPROILE 832
Db      2036 CGATCTACTACGACGAGCCCATTC 2060

RESULT 7
US-10-144-771-3346
: Sequence 3346, Application US/10144771
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig
: TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
: FILE REFERENCE: CLO01321
: CURRENT APPLICATION NUMBER: US/10/144, 771
: CURRENT FILING DATE: 2002-05-15
: NUMBER OF SEQ ID NOS: 47235
: SEQ ID NO 3346
: LENGTH: 3231
: TYPE: DNA
: ORGANISM: HUMAN
US-10-144-771-3346

Alignment Scores:
Pred. No.: 2,01e-141 Length: 3231
Score: 2010.00 Matches: 405
Percent Similarity: 62.00% Conservative: 91
Best Local Similarity: 50.62% Mismatches: 230
Query Match: 44.15% Indels: 74
DB: 9 Gaps: 19

US-09-634-252A-4 (1-832) x US-10-144-771-3346 (1-3231)
Qy      47 LEULEUVALLEULEULEULEUPROLEUALALASERSEARGLPROARGALATRPGLY 66

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Db      40 ATCGGGCTCTGCTGTGTACCGCTTCC-----CCGGCCGGCTTTGG 87
Qy      67 AlaAlaAlaPro--SerAlaProHisTrpAsnGluThrAlaGluLysAsnLeuGlyVal 85
Db      88 GCCCTGGGTCCCGAGAGAGCTCTGCACGTGAGAGAGCTCAGCC-----CATGTGGGG--- 138
Qy      86 LeuAlaAspGluAspAsnThrLeuGlnGlnAsnSerSerAsnIleSerTyrSerAsn 105
Db      139 -----AGCCCGAGAGCT 150
Qy      106 AlameGlnLysGluIleThrLeuProSerArgLeuIleTyrThrIleAsnGlnAspSer 125
Db      151 CCAGAGGCTCTAGGTCACAGAGCCAGCGGCTGTAGAGCAG---AGCTCCGGGGGA 207
Qy      126 GluSerProTyrHisValLeuAspThrTrpAlaArgHisGlnGlnIleHisAsnLysAla 145
Db      208 GAGGTCCGAAGAGCAGGTGGACACAGAGGTCGCCAGAGTCCGCCAGAGGGAGGAGCCT 267
Qy      146 ValHisLeuAlaGlnAlaSerPheGlnIleGluAlaPheGlySerTyrPheIleLeuAsp 165
Db      268 GTTCACCTGGCCCGAGGTGAGTTCGTATCCCGGCTTCGACTCAAACTTCACCTGGAC 327
Qy      166 LeuIleLeuAsnAsnGlyLeuLeuSerSerAspTyrValGluIleHisTyr---GluAsn 184
Db      328 CTGAGACTGACATCATCCTCTCTCTCTGCTGAGTATGTGAGCGCCACTTCACCGGAG 387
Qy      185 GlyLysProGlnTyrSerLysGly---GlyGluHisCysTyrTyrHisGlySerIleArg 203
Db      388 GGAACAAGACACACAGCAGCTGGGGCTGAGACCACTGACTACTACCTGGGAACCTCCG 447
Qy      204 GlyValLysAspSerLysValAlaLeuSerThrCysAsnGlyLeuHisGlyMetPheGlu 223
Db      448 GGGACCCACAGTCCTTCTGCTGCACTCTTACATGCCAGGGGCTGAGGGCTTCTCT 507
Qy      224 AspAspThrPheValTyrMetIleGluProLeuGlnLeuVal-----HisAspGluLys 241
Db      508 GATGGCAACTGACTTACATCGTAGAGCCTAAGAGATAGTGGCCCTGGGGACCCCA 567
Qy      242 SerThrGlyArgProHisIleIleGlnLysThr----- 252
Db      568 CAGGAGCCCTTCCGCCATTTACCGGAGCCCTCTCTCCAGCCCTTGATGC 627
Qy      253 -----LeuAlaGlyGlnTyrSerLysGlnMetLysAsnLeuThrMet 266
Db      628 AGGAGCCAGGCTCCCTGTTGCTGCTCCCGCCAGCTGCTGCCAAC----- 678
Qy      267 GluArgGlyAspGlnTrpProPheLeuSerGluLeuGlnTrpLeuLysArgArgLysArg 286
Db      679 -----TGCCCAAGCTA-----AGAAAGAAAGG 702
Qy      287 AlaValAsnProSerArgGly-----IlePheGluGlnMetLysTyrLeuGlnLeu 303
Db      703 CAGGTCCGC-----AGGGCCACCCACAGTGCACAGCAGACCAAGTATGTGAGTTG 756
Qy      304 MetIleValAsnAspHisLysThrTyrLysLysHisArgSerSerHisAlaHisThrAsn 323
Db      757 ATTGTATTCATGACCCACAGCTGTGTGACAGATGGGAGAGTGAAGTGTCTCACCAGC 816
Qy      324 AsnPheAlaLysSerValValAsnLeuValAspSerIleTyrLysGlnGlnLeuAsnThr 343
Db      817 AACTTTGCAAAATCTGTTGAACTGGACGTGATGATATACAGAGAACAGCTCAACACA 876
Qy      344 ArgValValLeuValAlaValGluThrTrpThrGluLysAspGlnIleAspIleThr 363
Db      877 AGAATTTCTGTGTGGCATGGAACGTGGCAGATGGGACAGATCCAGGTCCAGGAT 936
Qy      364 AsnProValGlnMetLeuHisGluPheSerLysTyrArgLysArg---IleLysGlnHis 382
Db      937 GACTACTGAGAGACCTGGCCGGCTTATGTCTACCGCGGAGGAGTCTCCGAGACC 996
Qy      383 AlaAspAlaValHisLeuIleSerArgValThrPheHisTyrLysArgSerSerLeuSer 402
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Db      997 AGTATGCCACCCACCTCTTCTCGGTTAGACCTTCCAAAGACCAAGCAGCGGGGGCGCC 1056
Qy      403 TyrPheGlyGlyValCysSerArgThrArgGlyValGlyValAsnGluTyrGlyLeuPro 422
Db      1057 TAGCTGGAGGAGCATGTTTACACTGTCCAGGGGTGAGGTGAGACAGATGATGAAACATG 1116
Qy      423 MetAlaValAlaGlnValLeuSerGlnSerIleuAlaGlnAsnLeuGlyIleGlnTrp--- 441
Db      1117 GGTGCCATGGCGTGAACCTGGGCCAGACGCTTAGGCGCAACACTTGGGCAATGATGGAAAT 1176
Qy      442 GluProSerSerArgLysProLysCysAspCysThrGluSerTrpLysGlyCysIleMet 461
Db      1177 AACGACCGGAGCTCAGACAGGGAGCGACTGCAAGTGTCCAGACATTTGGCTGGGCTGATCAG 1236
Qy      462 GluGluThrGlyValSerHisSerArgLysPheSerLysCysSerIleLeuGluTyrArg 481
Db      1237 GAGGACATCGGGCTTCATTTGCCCCCAAGTTTCCGGCTGACATGCACAAATTAACAAC 1296
Qy      482 AspPheLeuGlnArgGlyGlyValAlaCysLeuPheAsnArgProThrLysLeuPheGlu 501
Db      1297 CAATTTCGAGAGAGGAGGAGGAGGAGCTGCTTCAACAAGCCCTCAAGCTTTCGAGC 1356
Qy      502 ProThrGluCysGlyAsnGlyTyrValGluAlaGlyLeuGluCysAspCysGlyPheHis 521
Db      1357 CTTCCGAGAGTCCGAAACGGCTTCTGTGAGGCGGAGAGAGATGCGAGTCCGGTGGTG 1416
Qy      522 ValGluCysTyr-----GlyLeuCysCysLysLysCysSerLeuSerAsnGlyAla 538
Db      1417 CAGGAGTGCAGCCGACGAGGAGGCAACTGCTGCAAAAATGCACTTGACGCAAGCGCC 1476
Qy      539 HisCysSerAspGlyProCysCysAsnAsnThrSerCysLeuPheGlnProArgGlyTyr 558
Db      1477 ATGTGCAGCATGAGCTCTGTGTGCGCC-----TGCAAGTATGAGCCAGCAGGTTGC 1530
Qy      559 GluCysArgAspAlaValAsnGluCysAspIleThrGluTyrCysThrGlyAspSerGly 578
Db      1531 TCTTCCGGAAGACCGGTAATGAGTGCATTCGAGAGAGACCTGCACCGCGCTCAACG 1590
Qy      579 GlnCysProProAsnLeuHisLysGlnAspGlyTyrValAlaCysAsnGlnAsnGlnLysArg 598
Db      1591 CAGTGTCCCTTAACCTTCAACAGCTGACGAGCTTACTGTATCATGACGAGGCTGT 1650
Qy      599 CysTyrAsnGlyLysCysLysThrArgAspAsnGlnCysGlnTyrIleTrpGlyThrLys 618
Db      1651 TCGTATGAGAGCGCGCTGTAACCCGGAGCCGAGGCCAACCCATGGCCCATGCG 1710
Qy      619 AlaAlaGlySerAspLysPheCysTyrGluLysLeuAsnThrGluGlyThrLysGly 638
Db      1711 GCTGCG-----GATCGTTCTCTATGAGAACCTGAACGTGAGGAGGACAGAGCGTGA 1764
Qy      639 AsnCysGlyLysAspGlyAspArgTrpIleGlnCysSerLysHisAspValPheCysGly 658
Db      1765 AACTGTGACGCAAGGATGTGTTGGGTCCAGTGCAGTAAACAGATATGCTGTGCG 1824
Qy      659 PheLeuLeuCysThrAsnLeuThrArgAlaProArgIleGlnLeuGlnGlyIle 678
Db      1825 TTCTTCTGTCGTCACATCTCTGAGCTCCGGGCTTGGAGGATGTGGGGGCCATCAG 1884
Qy      679 IleProThrSerPheTyrHisGlnGlyArgValIleAspCysSerGlyAlaHisVal 698
Db      1885 AGCAGTGTCACTTTCACCAACAGGCGCAAGAGTGGACAGTGGAGGAGGCGCACGTGCAG 1944
Qy      699 LeuAspAspAspThrAspValGlyTyrValGluAspGlyThrProCysGlyProSerMet 718
Db      1945 CTACGCTATGCTCGACCTGACCTGAGTATGTGAGAGCAGCAGCGGCTTGGGCCAATC 2004
Qy      719 MetCysLeuAspArgLysCysLeuGlnIleGlnAlaLeuAsnMetSerCysProLeu 738
Db      2005 TTGTGCTAGTACCCCTCCAGCTCCAGCTCTTCAACCTTCAACACCTCCGCTGGA 2064
Qy      739 AspSerLysGlyLysValLysSerGlyHisGlyValLysSerAsnGluAlaThrCysIle 758
Db      2065 AGTGCAGAGCGAAGATCTCTCCATCATGGGTTTGGACAGCAAGAGGAGAGTATATC 2124
:::||||| ||||| |||

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[illegible]

Alignment Scores:	
Pred. No.:	2,77e-140
Score:	1994.00
Percent Similarity:	59.64%
Best Local Similarity:	45.95%
Query Match:	43.80%
DB:	8
US-09-634-252A-4 (1-832) x US-10-170-235-7480 (1-2875)	
	Length: 2875
	Matches: 403
	Conservative: 120
	Mismatches: 253
	Indels: 102
	Gaps: 19

[illegible]

Db	428	GACAGCGGGGTGCGGGGCGACCTCGGTGGCCGCCGACGTTGACATCATGTTGACCAAGCAAC	487
Qy	153	pheGlnIleGlnAlaPheGlySerLysPheIleLeuAspLeuIleLeuAsnAsnGlyLeu	172
Db	488	TTCCAGGTGAATGCCCTTTGGAAACGTCATTCATTTCTCGATGTCGTCTAATCATCATGATTGG	547
Qy	173	LeuSerSerAspTyrValGluIleHisTyrGluAsn---GlyLysProGlnTyrSerLys	191
Db	548	CTGTCTCTCGAATACATACATAGAGACACATTTGACATCGAGCAAGCATCTGGACATTAA	607
Qy	192	GlyGlyGlnHisCysTyrTyrHisGlySerIleArgGlyValLysAspSerLysValAla	211
Db	608	GGAGAGAGACACTGTTACTACAGAGGCCATTATCCGAGAAACCCGTGATTCATTGTTTGA	667
Qy	212	LeuSerTyrCysAsnGlyLeuHisGlyMetPheGluAspSPTHrPheValTyrMetIle	231
Db	668	TTGTCAACATGCCACAGCACTTCATGGAGTTCTATAGAGGGAACACACATCATTCATTT	727
Qy	232	GluProLeuGluLeuValHisAspGluLysSerTyrGlyArgPro-----His	247
Db	728	GAGCCA-----GAGAAATGACACTACATCAAGAGATTTCCATTTCAT	772
Qy	248	IleIleGlnLysThrLeuAlaGlyGlnTyrSerLys-----Gln	260
Db	773	TCAGTTTACAATTCACAGACTGTTTGAATTTTCTTGATGATCTTCCATCTGAATTTTCAG	832
Qy	261	MetLysAsnLeuThrMetGluArgGlyAspGlnTyrProPheLeuSerGlnLeuGlnTyr	280
Db	833	CAAGTAACATTTACTCATCAAA-----TTTATTTTGAACCAAGACCA	877
Qy	281	LeuLysArgArgLysArgAlaValAsnProSerArgGlyIlePheGlnGluMetLysTyr	300
Db	878	AAAGAGATAAACGCGACGCTTCGTGATCTCTCGTAATGTGAAGAAACCAATATAC	937
Qy	301	LeuGluLeuMetIleValAsnAspHisLysTyrTyrLysLysHisArgSerHisAla	320
Db	938	ATTGACACTGATGATTTGATGATCATCACCTTATGTTTAAACAAATCGCTTCCTGTGA	997
Qy	321	HisThrAsnAsnPheAlaLysSerValValAsnLeuValAspSerIleTyrLysGlnGln	340
Db	998	CATACCAATACCTATGCGCAATCTGTGGGAACATGCGCATGTTATATTAAGAAGCA	105
Qy	341	LeuAsnThrArgValValLeuValAlaValGluThrTyrThrGluLysAspGlnIleAsp	360
Db	1058	CTTAAGACACGAGATGATGTGTTCTCTATGGAACCTGGCGACATGCACAAATGTTGCC	111
Qy	361	IleThrThrAsnProValGlnMetLeuHisGlnPheSerLysTyrArgGlnTyr---Ile	379
Db	1118	ATATCTGAAATCCATTTGATCTACCTACCTAGTGAGTTTATGAATACAGAGGGATTTTATC	117
Qy	380	LysGlnHisAlaAspAlaValHisLeuIleSerArgValThrPheHisTyrLysArgSer	399
Db	1178	AAAGAGAAAGATGATGACAGCTTCACCTTTTTCGGGAAGTCATTTGAGAGTCGCGAGC	123
Qy	400	SerLeuSerTyrPheGlyGlyValLysSerArgThrArgGlyValGlyAlaAsnGluTyr	419
Db	1238	GGGCGAGCTTATATTGGTGGAATTGCTCGTTTGCTGAAGAGAGAGGCGCTGAATGAATTT	129
Qy	420	GlyLeuProMetAlaValAlaGlnValLeuSerGlnSerLeuAlaGlnAsnLeuGlyIle	439
Db	1298	GGGAAACATGATTTAATGGCTGTACACTTGGCCAGTCATTTAGCCCATATATTTGGTATT	135
Qy	440	GlnThrGluProSerSerArgLysProLys-----CysAspCysThrGlu	454
Db	1358	-----ATCTCAGACAAAAAGAAAGTTAGCAAGTGTGAATGTAAATCCGAGAC	1401
Qy	455	SerTyrGlyGlyCysIleMetGluIleThrGlyValSerHisSerArgLysPheSerLys	474
Db	1406	ACGTGTCGCGGTGCATATAGGAGACACACTGGCTATTATCTTCCATAAAGTTTACCCAG	1461
Qy	475	CysSerIleLeuGluTyrArgAspPheLeuGlnArgGlyGlyValAlaCysLeuPheAsn	494





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Db      668  TTGTCACATGCGCAGCACTTCATGGATGTCATGAGCGGAAACCAACATATCTCATT 727
Oy      232  GLUPROLEUGLULEVALHISAPLULYSSETHRGILYAIRGPRO-----HIS 247
Db      728  GAGCCA-----GAGAAATAAGACACTACTCAAGAGAGATTCCATTTCATTTTCA 772
Oy      248  ILEILEGLINLSTHLEUALAGLYGINTYRSERLYS-----Gln 260
Db      773  TCAGTTCAACAAATCCAGACTGTTTGAATTTCTTGATGATCTTCATCTCAATTTTCAG 832
Oy      261  METLYSASNLSTHMETCULARGELYSPGLINTYRPROPHLEUSERGLULEGINTYR 280
Db      833  CAAGTAACCATTTACTCCATCAAAA-----TTTATTTTGAACCAACAGAACCA 877
Oy      281  LEULYSARGARGLYAIRGALVALASNPROSERARGLYILEPHEGLULUMELLYSTYR 300
Db      878  AAAAGGAGCTAAACGGCAGCTTCGCGATATCTCTGTAATGTAGAACAGAACCAAAATAC 937
Oy      301  LEUGLULEUMELLEVALASNPASPHISLSTHRTYRSLYSHISARGSESRHISALE 320
Db      938  ATTGAACATGATGATGTGATGATCATCCTTATGTTAAACAAATCGCTTCGCTTGTA 997
Oy      321  HISTHRASNPHEALALYSSEVALVALASNLLEUALASPSERILETYRSLYGLIN 340
Db      998  CATACCAATACCTATGCAAAATCTGTGCGAACATGCGAGATTATATATAAGACAA 1057
Oy      341  LEUASNPTRARGVALVALLEUALVALALGINTHTTRTHGLULYSAPGLINILEASP 360
Db      1058  CTTAAGACGAGATGATGATGTTGTTGCTATAGAACCTGGCGACATGACAAAGTTTGC 1117
Oy      361  ILETHRTRASPPOVALGIMETLEUHSGLUPHESERLYSTYRARGINARG---ILE 379
Db      1118  ATATCTGAATAATCCATTTGATCCCTACCTGAGTTTATGAATACAGGAGGATTTTATC 1177
Oy      380  LYSGLINHSALASPALEVALHISLEULISERARGVALTHRPHEISTYRSLYASARG 399
Db      1178  AAAGGAAAGAGTGAAGCAGCTTCACCTTTTTCGGGAAGTCAAATTTAGAGTACCCGAG 1237
Oy      400  SERLESERTYRPHGLYGLYVALYLSSEARGTHARGLYVALGLYVALASNLGINTYR 419
Db      1238  GGGCAGCTGTATATGTTGGTGGATTTGCTGTCGTAAGAGAGAGCGCTGAATGTAATTT 1297
Oy      420  GLYLEUPROMELALVALALAGLVALLEUSERGINSERLEUALAGLINSLEUGLYILE 439
Db      1298  GGGAAACATGATTAATGGCTGTACACTTCCAGATCTATGATCCCATATATATGTTAT 1357
Oy      440  GLINTYRGLUPROSERSEARGLYSPROLYS-----CYSAPCYSTHARGLU 454
Db      1358  -----ATCTCAGACAAAGAAAGTACCAAGTGTCAATGTAAATCCGACGAC 1405
Oy      455  SEETPGLYGLYCYSILEMERGLULHTRGILYVALSERHISERARGLYSPHESERLYS 474
Db      1406  ACGTGCTCGGGTGCATATATGGAGACACTGGCTATATCTTCCTTAAAGATTCACCCAG 1465
Oy      475  CYSSERTILEUGLUTYRARGSPHELEUGLARGGLYGLYVALYLSYLSLEUPHEASN 494
Db      1466  TGTATATATTGAAGACTATCATCTCCGATAGTGAAGAGTGTCCTCCCTTTTCAAC 1525
Oy      495  ARGPROTHRLYSLEUPHGLUPROTHRGILYCYSGLYASNLGYTYRVALGLUALAGLY 514
Db      1526  AAACCTCTAAGCTTCTGATCTCTCTGAGTGTGCAATGAGCTTCATGAAGATGAGAG 1585
Oy      515  GLUCYSAPCYSGLYPHENISVALGLUCYSTYR-----GLYENYSCYSLYLS 531
Db      1586  GAGTGCTGATTTGTGAACCCCGCGCGAATGTGCTTGAAGAGACAGAGTGTGTAGAAGA 1645
Oy      532  CYSSERTLEUSERASNLVALAHISCYSSERASPGLYPROCYSSASNPANSTHRSARG 551
Db      1646  TGCACCTTGACCTCAAGACTGTCAATGACAGTGGCTTGTGCTGTA-----AGTGC 1699
Oy      552  LEUPHEGLINPROALIGLYTYRGLUCYSARGASPALEVALASNLUCYSPILLETARGLU 571

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Db      1700  AAGTTTCAGCTATGCGCAGCTGTGTCGCGAGAACAGTAATATGATGATATTCGTGAA 1759
Oy      572  TYRCYSSTRHRLYASPSERGLYGLINCYSPPROFASNLLEUHSLSYGLINSPGLIYVAL 591
Db      1760  ACGTGCTCAGGAATAATTAACCCAGCTGTCCTTATATATCTTAAATAAGATGATATTC 1819
Oy      592  CYSASNLINSNGLNYARGCYSTYRASNGLYGLYLSYLSYSTRHARGSPASNLGINTYR 611
Db      1820  TGTGATGCTGTTCAGGGAATTTGCTTGTGAGAGAGATGCCAAACAGAGATAGACAATGC 1879
Oy      612  GLINTYRILETRPGLYTHRLYSALALEGLYSERASPLYSPEHCYSTYRGLULYSLEUASN 631
Db      1880  AAATACATTTTGGGGGCAAAAGCTGACAGCATACAGCAAAATTTGCTATGAGAACTGAT 1939
Oy      632  THRGLUGLYTHRGILYULYSGLYASNCYSGLYLYSAPGLYASPARAGTTPILGLINCYS 651
Db      1940  ATTGAAGGAGCGGAGAGAGGTTAAGTGGGAAAGCAAGACACATGATACATGTCACAC 1999
Oy      652  LYSHISAPRYALPHECYSGLYPHELEUCYSTHRSASNLSTHARGALAPROARGILE 671
Db      2000  AAACGGATGCTGCTTTGCTGTTACCTTTTGTACCAATATGGCAATATCCCAAGCTT 2059
Oy      672  GLYGLINLEUGLINCGLYILELEPROTHRSERPHETYRHSGLNYARGVALILEASP 691
Db      2060  GGAACACTCGATGGAATAACATCATCTTACTTGCGCAGCAAGGAAGAACATTAAC 2119
Oy      692  CYSSERTGLYALHISVALLEUALASPARSPHRSPVALIGLYTYRVALGLIASPGLY 711
Db      2120  TGCAGTGCTGGCATGTGTTAAGCTTGAAGAAATGATATCATCTGCTATGCGAAGATGCG 2179
Oy      712  THRPROCYSLYPROSERMETCYSLEUASPARGYSCYSLAUGLINLEGLALALEU 731
Db      2180  ACACCTTGCTGTCCTCCCAATGATGCTGTAGAACACAGGTGCTTCTCGTGGCTTTTTC 2239
Oy      732  ASMETSERSECYSPROLEUASPSERLYSGLYVALYLSYSERGLYHISGLYVALCY 751
Db      2240  AACTTTAGTCTGCTGTCGACACAGTAAGAAAGCAGCTATTTCTCAGGAATAAGGATTGC 2299
Oy      752  SERASGLUALATHRCYSILIECYASPPHEHTRPRALAGLYTHRSAPCYSERTILEARG 771
Db      2300  AGTAATAGCTGAGATGTGTGTGAACAGACACATGAGTATGCTGATTC----- 2350
Oy      772  ASPROVALARGASNLLEUHSPPROLYSAPGLULGLYPROLYS----- 786
Db      2351  -----AACACTTACTTCCCTCACATATGATGCAAAAGACTGATATCACTGTC 2398
Oy      787  -----GLYPROSERALATHRASNLEULILEGLYSERILEALGLYALALEU 803
Db      2399  TCTGCGCAATGCTGTGCTGCGACCAATATCATATAGCCATAATGCTGCGCACCATTTTA 2458
Oy      804  VALALALELLEVALLEUGLYGLYTHRGILYTRPGLYRPHLYSASNLVALYS 820
Db      2459  GTGCTGCGCTCATATTAAGATATAGTGCAGGCTTATTAAGTAAGTGA 2509

RESULT 10
US-10-170-235-7479
: Sequence 7479, Application US/10170235
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig
: TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HU
: TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEROF
: FILE REFERENCE: CLO01380
: CURRENT APPLICATION NUMBER: US/10/170, 235
: CURRENT FILING DATE: 2003-03-17
: NUMBER OF SEQ ID NOS: 42514
: SEQ ID NO 7479
: LENGTH: 6753
: TYPE: DNA
: ORGANISM: HUMAN
US-10-170-235-7479

Alignment Scores:      8.94e-140      Length:      6753
Pred. No.:

```

Score: 1994.00  
 Percent Similarity: 59.64%  
 Best Local Similarity: 45.95%  
 Query Match: 43.80%  
 DB: 8  
 Matches: 403  
 Conservative: 120  
 Mismatches: 253  
 Indels: 102  
 Gaps: 19

US-09-634-252a-4 (1-832) x US-10-170-235-7479 (1-6753)

QY 1 MetLysProProGlySerSerSerArgLInProProLeuAla-----Gly 15  
 Db 12 CTCCCCCGCGAGGAGGAGCGTCCCGAGAGCAATCGACATCGACCGCGGAGGT 71  
 QY 16 CysSerLeu-----AlaGlyAlaSerCysGlyProGlnArgGlyPro 29  
 Db 72 TGCAGCGCCAGCGCGCGAGCAGCAGCGCGCGCGGTGGAGAGTGGCGCGGAGCC 131  
 QY 30 AlaGly-----SerValProAlaSerAlaProAla----- 39  
 Db 132 CGGGGGCGCGAGGAGGAGGAGGAGTCCGGCGCGCGCGCATGAGAGCTGAGCTTC 191  
 QY 40-----ArgThrProProCysArgLeuLeuValLeuLeuLeuPro 54  
 Db 192 GGGGAGCGCGGCTGAGCGAGCAGCAGCATGCGAG----- 224  
 QY 55 ProLeuAlaAlaSerSerArgProArgAlaTArgLysAlaAlaAlaProSer-----Ala 72  
 Db 225-----CGCAGTGGCTGTCTCGTCCGCTCTTCTTCTGCTGCTCT 260  
 QY 73 ProHisTyrAsnGlnThrAlaGlnLysAsnLeuGlyValLeuAlaAspGluAspAsnThr 92  
 Db 261 GTGTCCCTGAGACCTGCTCCGCGCGCGC--TGCAGCGAGCAGAGAGCGCTCATGATG 319  
 QY 93 LeuGlnGlnAsnSerSerSerAsnIleSerTyrSerAsnAlaMetGlnLysGlnIleThr 112  
 Db 320 GAGCTAGAGAGAGAGAGAGAAC-----CGCTTCGGGAGCGCGAGAGCATC 367  
 QY 113 LeuProSerArgLeuIleTyrTyrIleAsnGlnAspSerGluSerProTyrHisValLeu 132  
 Db 368 GTGCCACTGCGCCCATCTACCGCTCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 427  
 QY 133 AspThrLysAlaArgHisGlnGlnLysHisAsnLysAlaValHisLeuAlaGlnAlaSer 152  
 Db 428 GACAGCGGGGCTCGCGCGAGCCTCGGCGCGCGAGTGTACTGTGTGACCAAGAGAGC 487  
 QY 153 PheGlnIleGlnAlaPheGlySerLysPheIleLeuAspLeuIleLeuAsnAsnGlyLeu 172  
 Db 488 TTCAGGTGATGCTTGGACGTATCTCATCTCATCTCATCTCATCTCATCTCATCTCAT 547  
 QY 173 LeuSerSerAspTyrValGluIleHisTyrGluAsn-----GlyLysProGlnTyrSerLys 191  
 Db 548 CTGTCCCTCAATATACATAGAGAGAGACATGACATGAGAGAGAGAGAGAGAGAGAG 607  
 QY 192 GlnGlyGlnHisCysTyrTyrHisGlySerIleArgGlyValAlaLysAspSerLysValAla 211  
 Db 608 GAG 667  
 QY 212 LeuSerThrCysAsnGlyLeuHisGlyMetPheGluAspAspThrPheValTyrMetIle 231  
 Db 668 TTGTCAACATGAGCAG 727  
 QY 232 GlnProLeuGlnLeuValHisAspGlnLysSerThrGlnLysPro-----His 247  
 Db 728 GAGCA-----GAG 772  
 QY 248 IleIleGlnLysThrLeuAlaGlyGlnTyrSerLys-----Gln 260  
 Db 773 TCAGTTTACAAATCCAGACTGTTGAATTTTCTTGATGATCTTCATCTGAATTTTCA 832  
 QY 261 MetLysAsnLeuThrMetGluArgGlyAspGlnTyrProPheLeuSerGlnLeuGlnTyr 280  
 Db 833 CAAGTAACATTTATCTCCATCAAAA-----TTTATTTTGAAGCCAGAGCA 877  
 QY 281 LeuLysArgArgLysArgAlaValAsnProSerArgGlyIlePheGlnGluMetLysTyr 300

Db 878 AAAAGAGTAAGAGCGAGCTTCGATATCTCGTAATGTATAGAGAGAGAGAGAGAGAG 937  
 QY 301 LeuGlnLeuMetIleValAsnAspHisLysThrTyrLysLysHisArgSerSerHisAla 320  
 Db 938 ATTGAACGTATGATTTGTAATGATGATCATCTATGTTAAAGAGAGAGAGAGAGAGAG 997  
 QY 321 HisThrAsnAsnPheAlaLysSerValValAsnLeuValAspSerIleTyrLysGlnGln 340  
 Db 998 CATACCAATACACATGGAATATGTGTGATGATGATGATGATGATGATGATGATGATG 1057  
 QY 341 LeuAsnThrArgValValLeuValAlaValGluThrTyrThrGlnLysAspGlnIleAsp 360  
 Db 1058 CTTAAGACCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1117  
 QY 361 IleThrThrAsnProValGlnMetLeuHisGlnPheSerLysTyrArgGlnArg-----Ile 379  
 Db 1118 ATATCTAAATATCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1177  
 QY 380 LysGlnHisAlaAspAlaValHisLeuIleSerArgValThrPheHisTyrLysArgSer 399  
 Db 1178 AAAG 1237  
 QY 400 SerLeuSerTyrPheGlnGlyValLysSerArgThrArgGlyValGlnLysGlnTyr 419  
 Db 1238 GGGGAG 1297  
 QY 420 GlyLeuProMetAlaValAlaGlnValLeuSerGlnSerLeuAlaGlnAsnLeuGlyLe 439  
 Db 1298 GGGAG 1357  
 QY 440 GlnTyrGlnProSerSerArgLysProLys-----CysAspCysThrGln 454  
 Db 1358-----ATCTGAGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1405  
 QY 455 SerTyrGlyGlyCysIleMetGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG 474  
 Db 1406 AGCTGTGCGCGAG 1465  
 QY 475 CysSerIleLeuGlnLysArgAspPheLeuGlnArgGlyGlyGlyLysLeuPheAsn 494  
 Db 1466 TGTAAATATGAAAGATATGATGATGATGATGATGATGATGATGATGATGATGATG 1525  
 QY 495 ArgProThrLysLeuPheGlnProThrGlnCysGlyAsnGlyTyrValGlnAlaGlnGly 514  
 Db 1526 AAACCTTCAAGCTTCTGATCTCTGATCTCTGATCTCTGATCTCTGATCTCTGATCT 1585  
 QY 515 GluCysAspCysGlyPheHisValGluCysTyr-----GlyLeuCysCysLysLys 531  
 Db 1586 GAGTGTGATTTGTGAACCGCGCGAGATGTCTTGAAGAGAGAGAGAGAGAGAGAGAG 1645  
 QY 532 CysSerLeuSerAsnGlnLysSerAspGlyProCysCysAsnAsnThrSerCys 551  
 Db 1646 TGCACCTTGAATCAACATCTCATATCAGTACAGTCTTGTCTGTAA-----AAGTGC 1699  
 QY 552 LeuPheGlnProArgGlyTyrGlnCysArgAspAlaValAsnGluCysAspIleThrGln 571  
 Db 1700 AAGTTTCAAGCTATGCGACTGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1759  
 QY 572 TyrCysThrGlnGlnAspSerGlnCysProProAsnLeuHisLysGlnAspGlnTyrAla 591  
 Db 1760 AGCTGTCTGAG 1819  
 QY 592 CysAsnGlnAsnGlnLysArgCysTyrAsnGlyGluCysLysThrArgAspAsnGlnCys 611  
 Db 1820 TGTGATGAGGTTCAGAGAGATTTGCTTTGGAGAGAGATGCAAAACCGAGATGAGACATGC 1879  
 QY 612 GlnTyrIleTyrGlnLysAlaAlaGlySerAspLysPheCysTyrGlnLysLeuAsn 631  
 Db 1880 AAATACATTTGGCGGAG 1939  
 QY 632 ThrGlnGlyThrGlnLysGlnCysGlyLysAspGlnLysArgThrPheGlnCysSer 651





OY	146	ValHisLeuAlaGlnAlaSerPheGlnIleGluAlaPheGlySerLysPheIleLeuAsp	165
OY	147	:      :      :      :      :      :      :      :      :	166
Db	371	ACTGATGTTGACCAAGCAAGCTTCCAGGTGATGCTTTGGAAAGTCATTTCTGCAT	430
OY	166	LeuIleLeuAsnAsnGlyLeuLeuSerSerAspTyrValGluIleHisTyrGluAsn---	184
Db	431	GTCTGCTAAATTCATGATTTGCTGCTGCTGATATCATAGAGACATCTTGACATGGA	490
OY	185	GlyLysProGlnTyrSerLysGlyGlyLysHisCysTyrTyrHisGlySerIleArgGly	204
Db	491	GGCAAGACTGTGGAAGTTAAAGAGAGACACTGTACTACACAGGCGCATGTCCAGAGA	550
OY	205	ValLysAspSerLysValAlaIleuSerThrCysAsnGlyLeuHisGlyMetPheLeuAsp	224
Db	551	AACCTGCTATTTGTCATTTGCATTTGCACATGTCCAGGACTTCATAGGATGCTTCAT	610
OY	225	AspThrPheValTyrMetIleGlyProLeuGlyLeuValHisAspGlyLysSerThrGly	244
Db	611	GGGAACCCACATATTCATGTAGGCA-----GAAGAAATGACACTACT	655
OY	245	ArgPro-----HisIleIleGlnLysThrIleuAlaGlyLysTyrSerLys---	259
Db	656	CAAGAGATTTCCATTTTCATTTGATTTACAAATGCACAGCTGTGTAATTTCTTGAT	715
OY	260	-----GlyMetLysAsnLeuThrMetGluArgGlyAspLeuIlePro	273
Db	716	GATCTTCCATGTGAATTTCCACCAAGTAAATTCATTCACATAA-----	760
OY	274	PheLeuSerGlyLeuGlnIleThrLysAsnArgGlyAsnArgAlaValAsnProSerArgGly	293
Db	761	TTTATTTTGAAGCCCAAGCAAAAGAGAGTAAAGCGCATTCCTGCGATATCTCTGTAAT	820
OY	294	IlePheGlyGlyMetLysTyrTyrLeuGlyLeuMetIleValAsnAspHisLysThrTyrLys	313
Db	821	CTAGACAGAAAGCAACCAATACATGTAAGTACATGATTTGAAATGATCACCTTATGTTAA	880
OY	314	LysHisAsnArgSerSerHisAlaHisThrAsnAsnProAlaLysSerValYalAsnLeuVal	333
Db	881	AAACATCGGCTTTCCTGTTGACATACCAATACATGTGGAAATCTGTGTGTAACTATGCA	940
OY	334	AspSerIleTyrLysGlyGlyLeuAsnThrArgValAlaLeuValAlaValGluThrThr	353
Db	941	GATTTAATATATTAAGACCAACTTATAGACCCAGGATATGTTGGTTCATGGAACCTGG	1000
OY	354	ThrGlyLysAspGlnIleAspIleThrThrAsnProValGlyMetLeuHisGlyPheSer	373
Db	1001	GGCAGTCACACAAGTGTCCATATCTGAAATTCATGATCACACCTACGTCAGTTATAG	1060
OY	374	LysTyrArgGlnArg---IleLysGlnHisAlaAspAlaValHisLeuIleSerArgVal	392
Db	1061	AAATACAGAGAGGATTTATATCAAGAGAAAGATGTATGCAGTTCACCTTTTTCGGGAGAT	1120
OY	393	ThrPheHisTyrLysArgSerSerLeuSerGlyThrPheGlyGlyValCysSerArgThrArg	412
Db	1121	CAATTTGAGAGTACCGCGAGCGGGCGACCTTATATGTTGGATTTGCTCGTTGCTGAAA	1180
OY	413	GlyValGlyValAsnGlyTyrGlyLeuProMetAlaValAlaGlnValLeuSerGlnSer	432
Db	1181	GGAGGAGCGGTGATGATTTGGGAAACGTATTAATAGCGTTCACACTTCCCAAGTCA	1240
OY	433	LeuAlaGlnAsnLeuGlyIleGlnIleThrLysProSerSerArgLysProLys-----	449
Db	1241	TTTATCCCATTAATATTTGTATTT-----ATCTCAGACAAAGAAAGTTACCAAGT	1288
OY	450	-----CysAspCysThrGlySerThrGlyLysIleMetGlnGlyIleThrGlyAlaSer	467
Db	1289	GGTGATATTAATGCGAGGACACGTGCTCCGGGTGCTCAATAATGGAGACACCTGGCTATAT	1348
OY	468	HisSerArgLysPheSerLysCysSerIleLeuGlnTyrArgAspPheLeuGlnArgGly	487
Db	1349	CTTCTTAAAGAGTTTACCACAGTGAATATTTGAAGAGTATCATGACTCTCTGAATAGTGA	1408
OY	488	GlyLysAlaCysLeuPheAsnArgProThrLysLeuPheGlyProThrGlyCysGlyAsn	507

Db	1409	GGTGTGGCTGCCTTTTTCACAAACCTTCTAAAGCTTCTTAACTCCCTCCAGTGTGGCAAT	1466
Oy	508	GLTYTGAValGluAlaGluGluGluCysAspCysGlyPheHisValGluCysTyr-----	525
Db	1469	GGCTTCATTGAAACAGCGAGAGAGAGTGATGTGTGGAAACCCGGCCGAATGTGTCTTGAA	1528
Oy	526	---GlyLeuCysCysLysLysCysSerLeuSerAsnGlyAlaHisCysSerAspGlyPro	544
Db	1529	GGACCGAGACTTGTGTGAATAATGGCACCTTGTGACTCAAGACTCTCAATGGACATGACGGTCTT	1588
Oy	545	CysCysAsnAsnThrSerCysLeuPheGlnProArgGlyTyrGluCysArgAspAlaVal	564
Db	1589	TGCTGTAAA-----AACTGCAAGTTTTCAGCCTATGGCCACTGTGTGCCCGAAGACACTA	1642
Oy	565	AsnGluCysAspIleThrGluTyrCysThrCysAspSerGlyGlnCysProProAsnLeu	584
Db	1643	AATGATGTGTGATATTTCGTAAGAACGTCGACAGAAATTCACACAGATGTGTGCCCTAATATT	1702
Oy	585	HisLysGlnAspGlyTyrAlaCysAsnGlnAsnGlnGlyArgCysTyrAsnGlyLys	604
Db	1703	CATAAAAAGATGGATATTTCATGTGATGGTGTCCGGCAAAATTTGCTTTGGAGAGATGC	1762
Oy	605	LysThrArgAspAsnGlnCysGlnTyrIleTyrPheGlyThrLysAlaAlaGlySerAspLys	624
Db	1763	AAAAACGAGATAGACATATGCCAATATACATTTTGGGGGCAAAAGGTGATCAGCATCAGACAAA	1822
Oy	625	PheCysTyrGluLysLeuAsnThrGluGlyThrGluLysGlyAsnCysGlyLysAspGly	644
Db	1823	TATTGCTATGAGAAACGATATATTGGAAGGAGGAGGAAAGGGTAACTGTGGGAACACAAA	1882
Oy	645	AspArgTrpIleGlnCysSerLysHisAspValPheCysGlyPheLeuLeuCysThrAsn	664
Db	1883	GACACATGTGAATACAGTGCACAAACAGGATGTCTTGTGGTTACCTTTTGTGATACCAAT	1942
Oy	665	LeuThrArgAlaProArgIleGlyGlnLeuGlnGlyIleIleProThrSerPheTyr	684
Db	1943	ATTGGCAATATCCCAAGGCTTGGAGAACTCCATGTGAAATACACACTACTTTAGTTGTG	2002
Oy	685	HisGlnGlyArgValIleAspCysSerGlyAlaHisValValLeuAspAspThrAsp	704
Db	2003	CAGCAGAGAAACATTTAACTGCAGTGTGGCATGTTAAGCTTGAAGATGAGATGATAGAT	2062
Oy	705	ValGlyTyrValGluAspGlyThrProCysGlyProSerMetMetCysLeuAspArgLys	724
Db	2063	CTTGCGCTATGTGGAGATGGAGACACTTGTGCTCCCAAAATGATGTCTTGTGAACACAGG	2122
Oy	725	CysLeuGlnIleGlnAlaLeuAsnMetSerSerCysProLeuAspSerLysGlyLysVal	744
Db	2123	TGTCTTCTCTGTGGCTTCTTTCACTTTAGTACTTGTCTTGACACAGTAAAGAAAGGCATATT	2182
Oy	745	CysSerGlyHisGlyValCysSerAsnGluAlaThrCysIleCysAspPheThrTrpAla	764
Db	2183	TGCTCAGAGAAATGGAGTTTGCAGTAATAGCTGAAGTGTGTGTGAACAGACACTGATTA	2242
Oy	765	GlyThrAspCysSerIleArgAspProValArgAsnLeuHisProProLysAspGluGly	784
Db	2243	GGTTCTGATATGC-----AACACTACTCTCCACCAAAATGATAT	2281
Oy	785	ProLys-----GlyProSerAlaThrAsnLeuIleGly	796
Db	2282	GCAAAAGACTGTATACACTCTGTCTCGGCATAGTGTGTGGCACCAATATATCATATATAGC	2342
Oy	797	SerIleAlaGlyAlaIleLeuValAlaAlaIleValLeuGlyGlyThrGlyTyrPhe	816
Db	2342	ATATTGTCTGCGACACATTATTAGTCTGTGCTGACCTCATATTAGGAATAAATCGCTGGGGTTAT	2401
Oy	817	LysAsnValLysLysArgArg 823	
Db	2402	AAAAACTATGTGAGAACAGAGG 2422	

Mon Jun 2 10:41:06 2003

us-09-634-252a-4.p2n.rnpn

Page 18

job time : 1256 secs

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GenCore version 5.1.6  
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## OM protein - nucleic search, using frame\_plus.p2n model

Run on: June 1, 2003, 18:33:56 : Search time 99 Seconds  
(Without alignments)  
2577.324 Million cell updates/sec

Title: US-09-634-252a-4  
Perfect score: 4553  
Sequence: 1 MKPPGSSRRPPLAGCSLAC.....GMCFKNKKRRFDPTGGPI 832

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Xgapop 10.0, Ygapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Command line parameters:

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## Database :

- Issued Patents.NA:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	3621	79.5	2268	4	US-09-351-414-1
2	3007	66.0	2088	4	US-09-351-414-3
3	1978	43.4	3183	1	US-08-243-542-8
4	1978	43.4	3183	1	US-08-477-407-8
5	1978	43.4	3183	1	US-08-484-355-8
6	1862.5	40.9	2913	1	US-08-243-542-7
7	1862.5	40.9	2913	1	US-08-477-407-7
8	1862.5	40.9	2913	1	US-08-484-355-7
9	1843	40.5	2923	1	US-08-243-542-6
10	1843	40.5	2923	1	US-08-477-407-6
11	1843	40.5	2923	1	US-08-484-355-6
12	1293	28.4	1464	1	US-08-243-542-5

13	1293	28.4	1464	1	US-08-477-407-5	Sequence 5, Appl1
14	1293	28.4	1464	1	US-08-484-355-5	Sequence 5, Appl1
15	910	20.0	9278	1	US-08-243-542-9	Sequence 9, Appl1
16	910	20.0	9278	1	US-08-477-407-9	Sequence 9, Appl1
17	910	20.0	9278	1	US-08-484-355-9	Sequence 9, Appl1
18	897	19.7	3468	4	US-09-632-098-3	Sequence 3, Appl1
19	871	19.1	3431	4	US-09-632-098-1	Sequence 1, Appl1
20	854	18.8	2968	4	US-09-813-819-1	Sequence 1, Appl1
21	854	18.8	2968	4	US-09-920-048-1	Sequence 1, Appl1
22	829	18.2	2648	2	US-08-836-443-1	Sequence 1, Appl1
23	796	17.5	2251	2	US-08-836-443-2	Sequence 2, Appl1
24	784.5	17.2	2050	4	US-09-026-001A-5	Sequence 5, Appl1
25	773.5	17.0	2335	4	US-09-026-001A-9	Sequence 9, Appl1
26	767.5	16.9	2359	4	US-09-026-001A-17	Sequence 17, Appl1
27	750	16.5	2309	4	US-09-026-001A-13	Sequence 13, Appl1
28	748	16.4	2297	2	US-09-026-001A-7	Sequence 7, Appl1
29	740	16.3	2650	5	US-08-765-243-7	Sequence 7, Appl1
30	740	16.3	2650	5	PCT-US95-07295-7	Sequence 7, Appl1
31	737.5	16.2	1851	4	US-09-608-790-2	Sequence 2, Appl1
32	723.5	15.9	2288	4	US-09-026-001A-11	Sequence 11, Appl1
33	711	15.6	2373	1	US-08-264-101-1	Sequence 1, Appl1
34	711	15.6	2373	2	US-08-765-243-1	Sequence 1, Appl1
35	711	15.6	2373	5	PCT-US95-07295-1	Sequence 1, Appl1
36	697	15.3	2553	2	US-08-765-243-5	Sequence 5, Appl1
37	697	15.3	2553	5	PCT-US95-07295-5	Sequence 5, Appl1
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39	647	14.2	2406	4	US-09-632-098-5	Sequence 5, Appl1
40	612	13.4	1820	4	US-09-026-001A-15	Sequence 15, Appl1
41	588	12.9	1590	2	US-08-836-442-2	Sequence 2, Appl1
42	588	12.9	2056	2	US-08-836-442-1	Sequence 1, Appl1
43	517	11.4	1768	1	US-08-264-101-3	Sequence 3, Appl1
44	517	11.4	1768	2	US-08-765-243-3	Sequence 3, Appl1
45	517	11.4	1768	5	PCT-US95-07295-3	Sequence 3, Appl1

## ALIGNMENTS

RESULT 1  
US-09-351-414-1  
Sequence 1, Application US/09351414  
Patent No. 6265199  
GENERAL INFORMATION:  
APPLICANT: Sheppard, Paul O.  
APPLICANT: Baidur, Nand  
APPLICANT: Delsher, Theresa A.  
TITLE OF INVENTION: DISINTEGRIN HOMOLOG  
FILE REFERENCE: 98-29  
CURRENT APPLICATION NUMBER: US/09/351,414  
CURRENT FILING DATE: 1999-07-09  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 2268  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (3)...(2090)  
NAME/KEY: misc.feature  
LOCATION: (1)...(2268)  
OTHER INFORMATION: n = A,T,C or G  
US-09-351-414-1  
Alignment Scores:  
Pred. No.: 4.66e-316  
Score: 3621.00  
Percent Similarity: 99.70%  
Best Local Similarity: 99.70%  
Query Match: 79.53%  
DB: 4  
Length: 2268  
Matches: 654  
Conservative: 0  
Mismatch: 2  
Indels: 0  
Gaps: 0  
US-09-634-252a-4 (1-832) x US-09-351-414-1 (1-2268)

OY	132	LeuAspThrIysAlaValArgHisGlnGlnIleuLysHisAsnLysAlaValHisIleuValIleuAlaGlnAla	151
DB	27	CTTGACACAAAGCGCAGACACACCGCAAAACATTAATTAAGCGCTGCATCTGGCCCGCAGCA	86
OY	152	SerPheGlnIleGluAlaPheGlySerLysPheIleLeuAspLeuIleLeuAsnGlnGly	171
DB	87	AGCTTCCAGATTGAAGCCCTTGGCTCCCAATTCTTGGACTCTTACTGACCAATTCGT	146
OY	172	LeuLeuSerSerAspIlyrValGluIleHisIlyrGluAsnGlyLysProGlnIlyrSerLys	191
DB	147	TTGTTGTCTTCGTGATTATCTGAGATTCTACAGAAATATGGGAACACAGTACTCTAAG	206
OY	192	GlyGlyGluHisCysLysIlyrThrHisGlySerIleArgGlyAlaLysAspSerLysValAla	211
DB	207	GGTGAGAGACACTGTTACTACCATGGACATCGAGCGGCTCAAGAAGCTCAAGGTGGCT	266
OY	212	LeuSerThrCysAsnGlyLeuHisGlyMetPheGluAspAspThrPheValIlyrMetIle	231
DB	267	CTGTCAACCTGGCAATGGACTTCATCGGCAAGTTTGAGATATATACCTTCGTGTATATA	326
OY	232	GluProLeuGluIleuValHisAspGluLysSerThrGlyArgProHisIleIleGlnLys	251
DB	327	GAGCCACTAGAGCTGTTCTATGATGAGAAAGCAGAGCTGACCAATATATCCAGAA	386
OY	252	ThrIleAlaGlyIleIlyrSerLysGlnMetLysAsnLeuThrMetGluIlyrGlyAspGln	271
DB	387	ACCTTGGCAGAGCAGTATCTTAAGCAAAATCAGAAATCTCATATGAAAGAGGTACCAG	446
OY	272	ThrProPheLeuSerGluLeuGlnIlyrPheLysArgIlyrAspArgAlaValAspProSer	291
DB	447	TGGCCCTTCTCTGTGATTACAGTGGTTGAAAGAAAGAAAGAGAGCAGTGAATCATCA	506
OY	292	ArgGlyIlePheGluGluMetLysIlyrLysLeuGluIleuMetIleValAsnAspHisLysThr	311
DB	507	CGTGGTATATTTCAGAAATGAATATTTGGAACTTATGATTGTAATGATCACAAAGC	566
OY	312	TyrLysLysHisArgSerSerHisAlaHisThrAsnAspPheAlaLysSerValAlaAsn	331
DB	567	TATTAAGAAGCATCCCTCTTCTCAATGCACATCCAAACCACTTGGCAAAGCTCGGTGCAC	626
OY	332	LeuValAspSerIleTyrLysGlnGluLeuAsnThrArgValIleValLeuValAlaValGlu	351
DB	627	CTTGTGGATTTCTATTACAGAGAGCAGCTCAACACCAGGTTGCTCGTGGCTGTAGAG	686
OY	352	ThrTrpThrGluLysAspGlnIleAspIleThrThrAsnProValGlnMetLeuHisGlu	371
DB	687	ACCTGCACTGGAAGAGATCAGATTGACATCACCAACCAACCTGTGCAGATGCTCCATGAG	746
OY	372	PheSerLysTyrArgGlnArgIleLysGlnHisAlaAspAlaValHisIleuLieserArg	391
DB	747	TTTCCAAAAATCCCGCAGCGCATTTAAGCAGCATGTGCAGTGTGCACCTCATCTCGCG	806
OY	392	ValThrPheHisTyrLysArgSerSerLeuSerTyrPheGlyGlyAlaCysSerArgThr	411
DB	807	GTGCAATTCACATAAGAGAGACAGCTCGAATTACTTTGAAGGTGCTGTTCTCCACA	866
OY	412	ArgGlyValGlyValAsnGluIlyrGlyLeuProMetAlaValAlaGlnValLeuSerGln	431
DB	867	AGAGAGATTGGTGTGAATGATGATGCTTCCAAATGGCAGTGACACAAAGTATATCCAG	926
OY	432	SerLeuAlaGlnAsnLeuGlyIleGlnIlyrPheGluProSerSerArgLysProLysCysAsp	451
DB	927	AGCCGTGGCTCAAAACCTTGGAAATCCAAATGGGAACCTTTAGCGAAAGGCCAAATATGAC	986
OY	452	CysThrGluSerThrPheGlyCysIleMetGlnGluIlyrGlyAlaSerHisSerArgLys	471
DB	987	TTCACAGAAATCCCGGGGTGGCTGCATCATGAGAGAAACAGGGGTGCCATTTCGAAAA	1046
OY	472	PheSerLysCysSerIleLeuGluIlyrArgAspPheLeuGlnArgGlyGlyAlaCys	491
DB	1047	TTTTCAAATGCGACATTTTGGAGTATAGACACTTTTACAGAGAGAGGTGGAGCTGCG	1106

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Db	1107	CTTTTCAACAGCCCAACAAAGCTATTGTGAGCCACCGAATGTGGAAATGATACGTGAA	1166
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OY	532	CysSerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnThrSerCys	551
Db	1227	TGTTCCCTCTCCAAAGGGGCTCACTGCAGCAGCGGCGCTGCTGAACATACCTATGT	1286
OY	552	LeuphegiuProArGlyTYrGluCysArgAspAlaValAsnGluCysAspIleThrGlu	571
Db	1287	CTTTTTCAGCCACAGGGGTATGAATGCCGGGATGCTGTGAACGAGTGTATTTACTGA	1346
OY	572	TYrCysThrGlyAspSerGlyGluCysProProAsnLeuHisLysGlnAspGlyTYrAla	591
Db	1347	TATTGTACTGGAGACTCTGGTCACTGCCCAACAATTTCTATAGCAAGACGGATATGCA	1406
OY	592	CysAsnGlnAsnGlnGlyArgCysTYrAsnGlyLlucLysLysThrArgAspAsnGlnCys	611
Db	1407	TGCATTCAAATCAAGGCGCGCTGCTACAAATGGCAGTGCAGAACACAGACAGTGT	1466
OY	612	GlnTYrIleTYrGlyTYrHisLysAlaIaGlySerAspLysPheCysTYrGluLysLeuAsn	631
Db	1467	CAGTACATCTGGGAGCAACAAAGCTCCAGGCTCTACAAAGTTCGTATGAAAGCTGAAT	1526
OY	632	ThrGluGlyTYrGluLysGlyVAsnOCysGlyLysAspGlyAspArgTPPIleGlnCysSer	651
Db	1527	ACAGAAGGACCTGAspAspAspGAAACTGCGGGAAGATGGAGACGCGGTGATTCATGCAC	1586
OY	652	LysHisAspValPheCysGlyPheLeuLeuCysThrAsnLeuThrArgAlaProArgIle	671
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OY	672	GlyGlnLeuGlnGlyGluIleIleProThrSerPheTYrHisGlnGlyArgValIleAsp	691
Db	1647	GGTCACTTCAGGGGTGAGATCATTTCCAACTTCTCTACCATCAAGCCGGGTGATTGAC	1706
OY	692	CysSerGlyVAlaHisValLeuAspAspAspThrAspValGlyTYrValGluAspGly	711
Db	1707	TGCAGTGGTGGCCATGTACTTTAGATGATGATACGAGATGTGGCTATGTAGAGATGGA	1766
OY	712	ThrProCysGlyProSerMetMetCysLeuAspArgLysCysLeuGlnIleGlnAlaLeu	731
Db	1767	ACGGCAGTGGCCCGCTATGATGATGTTTATTCGGAATGCTCTCAAAATTCACACCTTA	1826
OY	732	AsnMetSerSerCysProLeuAspSerLysGlyLysValCysSerGlyHisGlyValCys	751
Db	1827	AATTTGAGCAGCTGTCCACTCGATTCGAAAGGTAAGTCTGTTCGGGCATCGGTGTGT	1886
OY	752	SerAsnGlnAlaThrCysIleCysAspPheThrTPRAlaGlyThrAspCysSerIleArg	771
Db	1887	AGTAAATACGCCACTTCATTTTGATATTCACCTGGGAGGACAGATGCGATGCCGG	1946
OY	772	AspProValArgAsnLeuHisProProLysAspGluGlyProLysGly	787
Db	1947	GATCCAGTAGGAACCTTCACCCGCCCAAGATGAAGAGACCCCAAGGGT	1994
RESULT 2			
US-09-351-414-3			
Sequence 3, Application US/09351414			
Patent No. 6265199			
GENERAL INFORMATION:			
APPLICANT: Sheppard, Paul O.			
APPLICANT: Baindur, Nand			
APPLICANT: Delsher, Theresa A.			
APPLICANT: Bishop, Paul D.			
TITLE OF INVENTION: DISINTEGRIN HOMOLOG			
FILE REFERENCE: 98-29			
CURRENT APPLICATION NUMBER: US/09/351,414			
CURRENT FILING DATE: 1999-07-09			

RESULT 2  
US-09-351-414-3  
Sequence 3, Application US/09351414  
Patent No. 6265199  
GENERAL INFORMATION:  
APPLICANT: Sheppard, Paul O.  
APPLICANT: Baird, Nand  
APPLICANT: Deisher, Theresa A.  
APPLICANT: Bishop, Paul D.  
TITLE OF INVENTION: DISINTEGRIN HOMOLOG  
FILE REFERENCE: 98-29  
CURRENT APPLICATION NUMBER: US/09/351,414  
CURRENT FILING DATE: 1999-07-09



[illegible][illegible]



QY 326 alysserValValasnleuValaspserIleTyrgLugInleuasnThraVala 346  
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QY 346 lleuValaValaIgtThrThraGluValaspGlnIleasplleThraProva 366  
Db 858 CCGTGTGGCTGCAACATGGGAGATGGGACAAATCCAGTGCAGTACCTCT 917  
QY 366 lGlnMetleuHisleuTheserIlyTrargGlnArg---lleysGlnHisAlaAspAl 385  
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QY 385 aValHisleuIleaserValThrPheHisIlyArgSerleuSerleuTrpPheI 405  
Db 978 CACCCACCTCTTCGCGGAGAGACCTTCAGAGACAGACAGAGGGGAGGCTACGTGG 1037  
QY 405 yglValaCysSerArgThraGlnValaGluValaAsnGluTrgIleuProMetaIaVa 425  
Db 1038 GGGCATATGCTCCCTGTCCTGAGGGGGGTGTCACAGAGTACGACATGGGGCGAT 1097  
QY 425 lAlaGlnValleuSerIleuSerleuAlaGlnAsnleuGlyIleGlnIleuProse 444  
Db 1098 GGGCGTACCTTCGCCAGACGCTGGAGACAGAACCTGGCATGTGAGACAAACACCG 1157  
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QY 464 rGlyValSerHisSerIlyPheSerIlyCysSerIleuGluTrgIleuAspPhele 484  
Db 1218 TGGGTTCCTACCTGGCCGCAAGTTCCTGTCGATGCATGCACATCAACACGTTTCT 1277  
QY 484 uGlnArgGlyGlyValaCysleuPheAsnArgProThrlsleuPheGluProThrl 504  
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QY 504 ucysGlyAsnGlyTyrgValaGluValaGluGluCysAspCysGlnPheHisValaGluCy 524  
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QY 524 sTyrg-----GlyleuCysCysIlyCysSerleuSerAsnGlnIleHisCysSe 541  
Db 1398 CACCCCGGAGGAGTGCACACTGCTGCAGAAATGCACCTGCTCACACGCGCATGTGAC 1457  
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Db 1458 CGAGCGGCTCTGCTGCGCGC-----TGCAGTACGAAACAGGAGGTGTGCTGCG 1511  
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QY 581 oProAsnleuHisIlyGlnAsnProIlyTrgIleuAsnGlnIleuArgCysTyrgAs 601  
Db 1572 GCGTAACTCTCACAGCTGAGGAGTGTACTGTACTGATGAGAGCGCGCTGCTACGG 1631  
QY 601 nGlyGluCysIlyThraGlnAsnGlnCysGlnIleTrpGlyThrlsAlaIaGln 621  
Db 1632 AGGTCCGTGCAAAACCGGAGACCGGAGCTGCCAGTCTTTGGGCGCATGCGGCTGCT 1689  
QY 621 ySerAspIlyPheCysTyrgIlyIleuAsnThrlGluIlyThrlsIlyAsnCysGln 641  
Db 1690 ----GATCGCTCTGCTACAGAGAGTGAATGTGAGGAGGAGCGAGCTGAGCTGCG 1745  
QY 641 yLysAspGlyAspArgTrpIleGlnCysSerIlyHisAspAlaPheIyScIlyPheIleu 661  
Db 1746 GCGCAAGGATCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1805  
QY 661 ucysThraAsnleuThraArgIleuProArgIleuGlnIleuGlnIlyIleuProth 681  
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QY 681 rSerPheThrlsGlnIlyArgValaIleAspCysSerGlyValaHisValaIleuAspAs 701  
Db 1666 CACCTTACACACAGGAGAGAGCTGAGCTGAGGAGGAGCCAGCTGAGCTGAGCGGA 1925  
QY 701 pasPThraPValaGlyTyrgValaGluAspGlyThrlProCysGlyProSerMetCysLe 721  
Db 1926 CGGCTGTGAGCTGAGCTGTGAGAGATGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1985  
QY 721 uAspArgIlyCysIleuGlnIleGlnAlaIleuAsnMetSerIlyProleuAspSerIly 741  
Db 1986 GGACCATTCGCTGCTGCGAGCTTCTGCTTCACTTCACTTCACTTCACTTCACTTCA 2045  
QY 741 sGlyValaCysSerGlnHisGlyValaCysSerAsnGlnIleuThrlsCysIleCysAspPh 761  
Db 2046 GCGCGGATTTGCTCCACACAGGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2105  
QY 761 eThrlPAlaGlyThraAspCysSerIleuArgAspProValaIrgAsnleuHisProPro 780  
Db 2106 AGACTGGACGAGCAAGACTGATTCATTCATTCATTCATTCATTCATTCATTCATTC 2165  
QY 781 -LysAspGluGlyProIlyGlyProSerAlaThraAsnleuIleIleGlySerIleAlaG 800  
Db 2166 GGAGCGGAGGATTAAGGATCCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2225  
QY 800 yAlaIleuValaIleuValaIleuValaIleuGlyIlyThrlTrpGlyPheIlyAsnVally 820  
Db 2226 GCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2285  
QY 820 slyAspArg 823  
Db 2286 CCGAGGAAG 2295

RESULT 4  
US-08-477-407-8  
Sequence 8, Application US/08477407  
Patent No. 5631351  
GENERAL INFORMATION:  
APPLICANT: NAKAMURA, YUSUKE  
TITLE OF INVENTION: MDC PROTEINS AND DNAS  
TITLE OF INVENTION: ENCODING THE SAME  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P. C.  
STREET: 2026 Rambling Road  
CITY: Kalamazoo  
STATE: Michigan  
COUNTRY: USA  
ZIP: 49008-1699  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage  
COMPUTER: IBM PC/XT/AT Compatible  
OPERATING SYSTEM: MS-DOS 5.0  
SOFTWARE: WordPerfect 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,407  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/243,542  
FILING DATE: 13-MAY-1994  
APPLICATION NUMBER: JP 5-136602  
FILING DATE: 14 MAY 1993  
APPLICATION NUMBER: JP 5-257455  
FILING DATE: 22 SEPTEMBER 1993  
APPLICATION NUMBER: JP 6-49904  
FILING DATE: 23 FEBRUARY 1994  
APPLICATION NUMBER: JP 6-73328  
FILING DATE: 12 APRIL 1994  
APPLICATION NUMBER: JP 6-84470  
FILING DATE: 22 APRIL 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Terrylene F. Chapman

```

1      REGISTRATION NUMBER: 32 549
2      REFERENCE/DOCKET NUMBER: Futrya Case 1313
3      TELECOMMUNICATION INFORMATION:
4      TELEPHONE: (616) 381-1156
5      TELEFAX: (616) 381-5465
6      INFORMATION FOR SEQ ID NO: 8:
7      SEQUENCE CHARACTERISTICS:
8      LENGTH: 3183 base pairs
9      TYPE: nucleic acid
10     STRANDEDNESS: double
11     TOPOLOGY: linear
12     MOLECULE TYPE: cDNA to mRNA
13     ORIGINAL SOURCE:
14     ORGANISM: Homo sapiens
15     IMMEDIATE SOURCE:
16     LIBRARY: human fetal brain cDNA library
17     FEATURE:
18     NAME/KEY: 3' UTR
19     LOCATION: 2308..3183
20     FEATURE:
21     NAME/KEY: CDS
22     LOCATION: 1..2307
23     OS-08-477-407-8

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QY	581	opRasInleuHisLysGlnAspGlyTYrValAlaCysAsnGlnAsnGlnGlyAspCysTYrAs	601
Db	1572	GCCTAACCTGCACACAGCTGAGCGGTACTACTGTGACCATATGACAGCGGCGCTGCTACGG	1631
QY	601	ngLYcLcysLysThrArgAspAsnGlnCysGlnTYrLleTYrPheGlyThrLYrAlaAlaG1	621
Db	1632	AGCTGCGCTGCACAAACCCGGGACCCGGACGTCCAGCTTCTTGGGGCCATCGCGCT--	1689
QY	621	ySerAspLysPheCysTYrGlyLysLeuAsnThrGlnGlyThrGlyLysGlyAsnGlyG1	641
Db	1690	----GATCGCTTCTGCTTACGAGAAAGCTGAATGTGAGGGGAGCGGAGCTGTGAGCTGTGG	1745
QY	641	LYAspAspLYAspArgTYrPheGlnCysSerLysHisAspValPheCysGlyPheLeuLe	661
Db	1746	GCACGAGGAGATCCCGGCTGGCTCCAGTGCAGTAAGACAGACACTGCTGTGCTTCCTCT	1805
QY	661	uCYsThrAsnLeuThrArgAlaProArgLleGlyGlnLeuGlnGlyLleLleProth	681
Db	1806	CTGTGTCAATCTCTGTGAGCTCTCTCGGCTCGATGAGGACCTGTGTGAGACATCACTAGTGT	1865
QY	681	rSerPheTYrHisGlnGlyArgValLleAspCysSerGlyValHisValLleuAspAs	701
Db	1866	CACCTTCTACACACAGGAGCAAGAGCTGTGACTGCAGGGGAGGCCACTGTGACGTGGCGA	1925
QY	701	pAspThrAspValGlyTYrValGluAspGlyTYrProCysGlyProSerMetMetCysLe	721
Db	1926	CGCGCTCGACCTGACGTACGTATGTGAGAGATGACACAGCTCGCGGCTTACATGTTGTGCT	1985
QY	721	uAspArgLYcysLeuGlnLleGlnAlaLeuAsnMetSerSerCysProLeuAspSerLY	741
Db	1986	GGACCATTCGCTGCTGCCACGCTTCTGCTTCACTTCACTTCACTGCGCGGACATGGGGA	2045
QY	741	sgLYAspValCysSerGlyHisGlyValCysSerAsnGluLathrCysLleCysAspPh	761
Db	2046	CGCGCTGATTTGCTCCACACACGGGGGTCTGACGACATGAAGGAAGTCACTGTGCACC	2105
QY	761	eThrTYrAlaGlyThrAspCysSerLleArgAspProValArgAsnLeuHisProPro--	780
Db	2106	AGACTGGACGACGAAAGACTGCACTATTCATCAATACCCCTGCCCCAGTCCGCCACCGGG	2165
QY	781	LYAspGlnGlyProLYsGlyProSerAlaThrAsnLeuLleLleGlySerLleAlaG1	800
Db	2166	GGACAGCGAGAGATATAAGTCTCCACGCGGACACCAATCATCTATGCTGCATCGCTGG	2225
QY	800	YAlaLleLeuValAlaAlaLleValLeuGlyGlyThrGlyTYrPGLyPheLYsAsnValLY	820
Db	2226	GGCGTCTCTGCTTCCAGCCATCTGCTGGGCGGACGGGCTGGGGAATTTAAACAATTTCG	2285
QY	820	sLYsArgArg 823	
Db	2286	CCGAGGAAG 2295	
RESULT 5			
US-08-484-355-8			
: Sequence 8, Application US/08484355			
: Patent No. 5705341			
GENERAL INFORMATION:			
APPLICANT: NAKAMURA, YUSUKE			
APPLICANT: EMI, MITSURU			
TITLE OF INVENTION: MDC PROTEINS AND DNAs			
TITLE OF INVENTION: ENCODING THE SAME			
NUMBER OF SEQUENCES: 20			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.			
STREET: 2026 Rambling Road			
CITY: Kalamazoo			
STATE: Michigan			
COUNTRY: USA			
ZIP: 49008-1699			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage			
COMPUTER: IBM PC/XT/AT Compatible			
OPERATING SYSTEM: MS-DOS 5.0			

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1 SOFTWARE: Mordperfect 5.0
2 CURRENT APPLICATION DATA:
3 APPLICATION NUMBER: US/08/484,355
4 FILING DATE: 07-JUN-1995
5 CLASSIFICATION: 536
6 PRIOR APPLICATION DATA:
7 APPLICATION NUMBER: US 08/243,542
8 FILING DATE: 13-MAY-1994
9 APPLICATION NUMBER: JP 5-136602
10 FILING DATE: 14 MAY 1993
11 APPLICATION NUMBER: JP 5-257455
12 FILING DATE: 22 SEPTEMBER 1993
13 APPLICATION NUMBER: JP 6-49904
14 FILING DATE: 23 FEBRUARY 1994
15 APPLICATION NUMBER: JP 6-73328
16 FILING DATE: 12 APRIL 1994
17 APPLICATION NUMBER: JP 6-84470
18 FILING DATE: 22 APRIL 1994
19 ATTORNEY/AGENT INFORMATION:
20 NAME: Terrylene F. Chapman
21 REGISTRATION NUMBER: 32,549
22 REFERENCE/DOCKET NUMBER: Futuya Case 1313
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: (616) 381-1156
25 TELEFAX: (616) 381-6455
26 INFORMATION FOR SEQ ID NO: 8:
27 SEQUENCE CHARACTERISTICS:
28 LENGTH: 3183 base pairs
29 TYPE: nucleic acid
30 STRANDEDNESS: double
31 TOPOLOGY: linear
32 MOLECULE TYPE: cDNA to mRNA
33 ORIGINAL SOURCE:
34 ORGANISM: Homo sapiens
35 IMMEDIATE SOURCE:
36 LIBRARY: human fetal brain cDNA library
37 FEATURE:
38 NAME/KEY: 3' UTR
39 LOCATION: 2308..3183
40 FEATURE:
41 NAME/KEY: CDS
42 LOCATION: 1..2307
43 US-08-484-355-8
44
45 Alignment Scores:
46 Pred. No.: 5,78e-168 Length: 3183
47 Score: 1978.00 Matches: 401
48 Percent Similarity: 61.6% Conservative: 95
49 Best Local Similarity: 49.88% Mismatches: 233
50 Query Match: 43.44% Indels: 76
51 DB: 1 Gaps: 17
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53 US-09-634-252A-4 (1-832) x US-08-484-355-8 (1-3183)
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55 Oy 46 LeuLeuLeuValLeuLeuLeuLeuProProlLeuAlaIlaSerSerArgProAla--- 64
56 ||||||| ||||| || | || |||
57 Db 34 CTGCTGTTCGGCTGCTCCGCCACCGCCGGCTTGGACCACAAGCTCTGTCGAGCTCG 93
58 |||||||
59 Oy 65 ---TrpGlyVala-----AlaIalProSerAlaPronHisTrpAsnGluThiAla 79
60 ||||| ||| |||||
61 Db 94 CGATCGGGGGGCGTTACCSCCAGCTGGAGAGCCACGAGGCCCT----- 135
62 ||||| ||| |||||
63 Oy 80 GluLysAsnLeuGlyValLeuAlaAspGluAspAsnThrLeuGlnGlnAsnSerSer 99
64 -----
65 Db 135 ----- 135
66
67 Oy 100 AsnIleSerTySerAsnAlaMetGlnLysGluIleThrLeuProSerArgLeuIleTy 119
68 ||||| ||||| ||||| ||||| |||||
69 Db 136 -----GAGGTCAcGGAACCCAGCCGCTGTGATTAGC 165
70 ||||| ||||| ||||| ||||| |||||
71 Oy 120 TyrIleAsnGlnAspSerGluSerProTyrHisValLeuAspThrLysAlaArgHisGln 139
72 ||||| ||||| ||||| ||||| |||||
73 Db 166 GAG----AGCTCCCGGGGAGAGGTCCGAAAGCAGCACGTGGACACAAAGGATCCGCAGGAG 222
74 ||||| ||||| ||||| ||||| |||||

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OY 140 GlnLysHisAsnLysAlaValHisLeuAlaGlnAlaSerPheGlnIleGluAlaPheGly 159  
DB 223 CCACAGAGGGGGCCCGCTGTCATCTGGCCAGAGTTCGTGATCCAGCCCTTAAC 282  
OY 160 SerLysPheIleLeuAspLeuIleLeuAsnGlyLeuLeuSerSerAspTyrValGlu 179  
DB 283 TCMAACTTCACCCCTGGACCTGAGTGAACCAACCACTCTCTCTCCATACATCTGGAG 342  
OY 180 IleHisTyr-----GluAsnGlyLysProGlnTyrSerLysGly---GlyGluHisCysTyr 197  
DB 343 GCCCACTTCAGCCGGGAGGGAGGCAACACCCAGACACACCGGGCGGAGACCACTGTAC 402  
OY 198 TyrHisGlySerIleArgGlyValLysAspSerLysValAlaLeuSerThrCysAsnGly 217  
DB 403 TACAGAGGGGAACCTCCGGGGGAACCCGACCTCTCCGCGCCCTCCACCTCCAGAGGG 462  
OY 218 LeuHisGlyMetPheGluAspAspThrPheValTyrMetIleGluProLeuGluVal 237  
DB 463 CTGCATGGGGTCTCTCTGATGGAACTTGACTTACATGTGGAGCCCAAGAGGTGCT 522  
OY 238 -----HisAspGluLysSerThrGlyArgProHisIleIleGlnLysThrLeuAlaGly 255  
DB 523 GACCTTGGGGAGCCCTCAGAGACCCCTCCCACTTACCTTACCGGACCCCTCTCT 581  
OY 256 GlnTyrSerLysGlnMetLysAsnLeuThrMetGluArgGlyAspGlnTyrPro-PheLe 275  
DB 582 CCCAGATCCCTCGGATG-----CAGGAAACCAAGGCTCTGTTGCG 623  
OY 275 uSerGluLeuGlnThrLeuLys-----ArgArgLysArgAlaValAs 289  
DB 624 TGTGCTGCCATCGCTCTCCAAACCGCGGAGGCTGAGAAAGGAGAGGTCCG 683  
OY 289 nProSerArgGly-----IlePheGluGlnMetLysTyrLeuGluLeuMetIleVal 306  
DB 684 C-----CGGGGCAACCTCAGTGCACAGTGAACCAAGTATGAGTATGTCAT 737  
OY 306 LAsnAspHisLysThrTyrLysHisArgSerSerHisAlaHisThrAsnAspPheAl 326  
DB 738 CAACGACACACAGCTGTTCAGCAGATGCGACACTCGGTGCTCCACCACTTTC 797  
OY 326 LysSerValValAsnLeuValAspSerIleTyrLysGlnLeuAsnThrArgValAla 346  
DB 798 CAGTGGTGGTGAACCTGGCCGATGTGATACAGAGAGAGCTCAACCTCCATCGT 857  
OY 346 IleValAlaValAlaGluThrTyrThrGluLysAspGlnIleAspIleThrThrAsnProVal 366  
DB 858 CTGTGTTGCCATGGAAACATGGGACATGGGACAAATCCAGTGCACCTCTCT 917  
OY 366 LglMetLeuHisGluPheSerLysTyrArgGlnArg---IleLysGlnHisAlaAspAl 385  
DB 918 GGAACACCTGGCCCGGCTCATGTCTACCGAGGAGGAGGTCTGCTGAGCCAGTAATGC 977  
OY 385 aValHisLeuLeuSerArgValAlaThrPheHisTyrLysArgSerSerLeuSerTyrPheG 405  
DB 978 CACCACTCTCTTCGCGGAGAGACCTTCAGAGCAGAGAGCGGGGAGAGCTAGCTGGG 1037  
OY 405 yGlyValCysSerArgThrArgGlyValAlaGlyValAsnGluTyrGlyLeuProMetAlaVal 425  
DB 1038 GGGCATATGCTCCCTGCTCCAGGGGGGGGTGTGAACAGTAACGCAACATGGGGGCAT 1097  
OY 425 lAlaGlnValLeuSerGlnSerLeuAlaGlnAsnLeuGlyIleGlnTyrP-----GluProSe 444  
DB 1098 GGCCCTGACCTTGGCCAGAGCGTGGAGACNACTGGGCAATGTGGAAACACCGG 1157  
OY 444 rSerArgLysProLysCysAspCysThrGlnSerTyrGlyGlyCysIleMetGluGluThr 464  
DB 1138 GAGCTCGGAGGAGGAGTGCAGATGTCCAGACATCTGGCTGGCTCATCATGAGAGAC 1217  
OY 464 rGlyValSerHisSerArgLysPheSerLysCysSerIleLeuGluTyrArgAspPheLe 484  
DB 1218 TGGGTTTCTACCTGGCCCGCAAGTCTCTGCTGAGCATGCAAGATACACCAAGTTTCT 1277

OY 484 uGlnArgGlyGlyGlyAlaCysLeuPheAsnArgProThrLysLeuPheGlnProThrG 504  
DB 1278 GCAGAGGGGTGTGACACTGCTCTTCACACACCCCTCAAGGTCTGAGCCCCACAGA 1337  
OY 504 uCysGlyAsnGlyTyrValAlaGluAlaGluGluCysAspCysPheHisValGluCys 524  
DB 1338 GTGCGGAAACGGCTTCGGAGGAGGAGGAGATGTCACACTCGGCTCGGTGAGAGATG 1397  
OY 524 sTyr-----GlyLeuCysCysLysLysCysSerLeuSerAsnGlyAlaHisCysSe 541  
DB 1398 CAGCCCGCAGGTGGCACTGTGTGACAAATGCAACCTGACTCAGACGCATGTGAG 1457  
OY 541 rAspGlyProCysCysAsnAsnThrSerCysLeuPheGlnProAlaArgGlyTyrGluCysArg 561  
DB 1458 GCAGGGGCTCTGCTGCGCCG-----TGCAGTACAGCAACACGCGGTGTCTCTGCG 1511  
OY 561 gAspAlaValAsnGluCysAspIleThrGlnTyrCysThrGlyAspSerGlyGlnCysPr 581  
DB 1512 AGAGCGCTGAAACGAGTGCAGATCGCGGAGACTGCACCGGGGACTCAGCCACTGCGC 1571  
OY 581 oProAsnLeuHisLysGlnAspGlyTyrAlaCysAsnGlnAsnGlnGlyArgCysTyrAs 601  
DB 1572 GCCTAACCTGCACAACTGGAGGTTACTAGTACATGTCAGACAGGCGCTGCTACCG 1631  
OY 601 nGlyGluCysLysThrArgAspAsnGlnCysGlnTyrIleTyrPglTyrThrLysAlaAlaG 621  
DB 1632 AGCTCGCTCAAAACCCGGGACCGGACGTCAGGTTCTTGGGGCATGCGGCTCT-- 1689  
OY 621 ySerAspLysPheCysTyrGluLysLeuAsnThrGlnGlyThrGluLysGlyAsnGly 641  
DB 1690 ---GATCGCTTGTGTACAGAACTGAAATGTGAGAGGGAGGAGCGAGCGGTGCG 1745  
OY 641 LysAspGlyAspArgTyrIleGlnCysSerLysHisAspValPheCysGlyPheLeuLe 661  
DB 1746 GCCCAAGGATTCGGGGTCCAGTACAGTACAGAGAGCTCTGTGCTGCTCTCTCT 1805  
OY 661 uCysThrAsnLeuThrArgAlaProArgIleGlyGlnLeuGlnGlyGluIleLeuProTh 681  
DB 1806 CTGTGTCAACATCTCTGAGCTCTCGCTAGGGAGACTGTGGAGACATCACTAGTCT 1865  
OY 681 rSerPheThrHisGlnGlnArgValAlaAspCysSerGlyAlaHisValValLeuAspAs 701  
DB 1866 CACTCTTACACACAGGCAAGAGCTGAGCTGAGGAGGAGGCGCAGCTGACGTGCGGA 1925  
OY 701 pAspThrAspValGlyTyrValAlaGluAspGlyThrProCysGlyProSerMetCysLe 721  
DB 1926 CGGCTGACCTGAGCTATGTGAGAGATGGACACGCTCGGGGCTTAACATGTTGTCCT 1985  
OY 721 uAspArgLysCysLeuGlnIleGlnAlaLeuAsnMetSerSerCysProLeuAspSerLy 741  
DB 1986 GGACCATCGCTGCTGCGACGCTTCTCACTTACAGCACTGCCCCGGCACTGGGGA 2045  
OY 741 sGlyLysValCysSerGlyHisGlyValLysSerAsnGluAlaThrCysIleCysAspPh 761  
DB 2046 GCGCGGATTCCTCCACCAACGAGGTGTGAGCAATGAAGGAATGATCATCTGTCAGCC 2105  
OY 761 eThrTrpAlaGlyThrAspCysSerIleArgAspProValArgAsnLeuHisProPro-- 780  
DB 2106 AGACTGACAGCAAAAGACTCAGATTCATACCCCTGCGCCACGTCGCCACACAGCGG 2165  
OY 781 -LysAspGluGlyProLysGlyProSerAlaThrAsnLeuIleIleGlySerIleAlaG 800  
DB 2166 GGAGACGAGAGATTAAGGTCCAGCGGCAACCAACATCATGTGGCTCATTCGCTGG 2225  
OY 800 yAlaIleLeuValAlaAlaIleValAlaGluGlyGlyThrGlyTyrPglTyrPheLysAsnVally 820  
DB 2226 GCGTGTCTGTGCTGACCATGTCTCTGGCGGACGCGGCTGGGATTAATAAACATTCG 2285  
OY 820 sLysArgArg 823  
DB 2286 CCGAGGAAGG 2295

RESULT 6

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US-08-243-542-7
: Sequence 7, Application US/08243542
: Patent No. 5552526
: GENERAL INFORMATION:
: APPLICANT: NAKAMURA, YUSUKE
: APPLICANT: : EMI, MITSURU
: TITLE OF INVENTION: MDC PROTEINS AND DNAS
: TITLE OF INVENTION: ENCODING THE SAME
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FLYNN, THEIL, BOUTELL & TANIS P.C.
: STREET: 2026 Rambling Road
: City: Kalamazoo
: STATE: Michigan
: COUNTRY: USA
: ZIP: 49008-1699
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
: COMPUTER: IBM PC/XT/AT Compatible
: OPERATING SYSTEM: MS-DOS 5.0
: SOFTWARE: Wordperfect 5.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/243,542
: FILING DATE:
: CLASSIFICATION: 530
: PRIORITY INFORMATION:
: APPLICATION NUMBER: JP 5-136602
: FILING DATE: 14 MAY 1993
: APPLICATION NUMBER: JP 5-257455
: FILING DATE: 22 SEPTEMBER 1993
: APPLICATION NUMBER: JP 6-49904
: FILING DATE: 23 FEBRUARY 1994
: APPLICATION NUMBER: JP 6-73328
: FILING DATE: 12 APRIL 1994
: APPLICATION NUMBER: JP 6-84470
: FILING DATE: 22 APRIL 1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Teriyence F. Chapman
: REGISTRATION NUMBER: 32 549
: REFERENCE/DOCKET NUMBER: Furuya Case 1313
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (616) 381-1156
: TELEFAX: (616) 381-5465
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2913 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: IMMEDIATE SOURCE:
: LIBRARY: human fetal brain cDNA library
: FEATURE:
: NAME/KEY: 5' UTR
: LOCATION: 1..27
: FEATURE:
: NAME/KEY: 3' UTR
: LOCATION: 2038..2913
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 28..2037
: US-08-243-542-7
:
: Alignment Scores:
: Pred. No.: 1,24e-157 Length: 2913
: Score: 1862.50 Matches: 360
: Percent Similarity: 66.77% Conservative: 91
: Best Local Similarity: 55.22% Mismatches: 193
: Query Match: 40.91% Indels: 33
: Gaps: 13

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US-09-634-252A-4 (1-832) x US-08-243-542-7 (1-2913)

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0Y	187	ProGlnTyrSerLysGly---GlyGluHisCysTyrTyrHisGlySerLeuArgGlyAla	205
Db	97	ACCCAGCACACACCGGGGCTGGAAACCACTGCTACTACAGGGAAGCTCCGGGGAGAC	156
0Y	206	LysAspSerLysValAlaLeuSerThrCysAsnGlyLeuHisGlyMetPheGluAspAsp	225
Db	157	CCGACACTCTTGGCGCCCTCTCCACACCTGCCAGGGGCTGCATGGGGTCTTCTCATATGG	216
0Y	226	ThrPheValTyrMetIleGluProLeuGluLeuVal-----HisAspGluLysSerThr	243
Db	217	AACTTGATGATCATCATCTGGAGCCCCCAAGAGGGCTGGACCTTGGAGGCCCTCAGGA	276
0Y	244	GlyArgProHisIleIleGlnLysThrLeuAlaGlyGlnTyrSerLysGlnMetLysAsn	263
Db	277	CCCCCTCCCACTCATTTACCGGACCCC-TCCTCTCCAGATCCCTCCGATG-----	329
0Y	264	LeuThrMetGluArgGlyAspGlnIlyPro-PheLeuSerGluLeuGlnTyrLeuLys--	282
Db	330	-----CAGGAAACCAAGGCTGCTTTTCTGCTGCTGCCCTCCAGTCCGCTCTCC	377
0Y	283	-----ArgArgLysArgAlaValAsnProSerArgGly-----I	294
Db	378	AAACCGCGCGAGCTGAGAGGAAAGGACAGTCCGC-----CGGGGCACTTCACAGT	431
0Y	294	ePheGlnGluMetLysTyrLeuGlnLeuMetIleValAsnAspHisLysThrTyrLysLys	314
Db	432	GCACAGTAAACCAAGTATGTCGACCTAAATGTGATCAACGCCACCACTGCTTGCAGCA	491
0Y	314	SHiArgSerSerHisAlaHisThrAspAsnPheAlaLysSerValAlaAsnLeuValAs	334
Db	492	GATCGGACAGTCGGGTGCTCCACCAAGCACTTTGCCAAGTCCTGGTGAACCTGGCCGA	551
0Y	334	pSerIleTyrLysGlnLeuAsnThrArgValAlaLeuValAlaValGluThrTyrPth	354
Db	552	TGTGATATACAGGAGCAGCTCACACATCGCATGCTCTGGTTCCTCATGAAACATGGGC	611
0Y	354	rGluLysAspGlnIleAspIleThrThrAsnProValGlnMetLeuHisGluPheSerLys	374
Db	612	AGATGGGAGCAAGATCCAGTGCAGAGATGACCTCTCGAGAGACCTCGCCGCTCATGCT	671
0Y	374	sTyrArgGlnArg---IleLysGlnHisAlaAspAlaValHisLeuIleSerArgValTh	393
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0Y	393	rPheHisTyrLysArgSerSerLeuSerTyrPheGlyValLysSerArgThrArgG1	413
Db	732	CTTCCAGAGCACAGACACCGGGGACGCTTACGTGGGGGACATATGCTCCCTGTCCATGG	791
0Y	413	yValGlyValAsnGlyTyrGlyLeuProMetAlaValAlaGlnValLeuSerGlnSerLe	433
Db	792	CGGGGCTGTGAACGATCAGCGCAACATGGGGCGATGGCCGAGACCTTCCCAAGACCT	851
0Y	433	uAlaGlnAsnLeuGlyIleGlnTyr---GluProSerSerArgLysProLysCysAspCy	452
Db	852	GGGACAGAACCTGGGCATGATGATGAACAAACCCGAGGCTCCGACGGGACTGCACAGC	911
0Y	452	sThrGluSerTrpGlyGlyCysIleMetGlnGluThrGlyAlaSerHisSerArgLysPh	472
Db	912	TCCAGACATCTGGCTGGGCTGCATCATGGAAGACACTGGGTTCATACCTGCCCGAAGTT	971
0Y	472	eSerLysCysSerIleLeuGlnTyrTyrArgAspPheLeuGlnArgGlyGlyAlaCysLe	492
Db	972	CTCTCGCTGACGATCGACAGTACAAACACTTTCTGCAGAGAGGTGTGGCAGCTGCCT	1031
0Y	492	uPheAsnArgProThrLysLeuPheGluProThrGluCysGlyAsnGlyTyrValGluAl	512
Db	1032	CTTCAACAAGCCCTCAAGCTCTGAGACCCCAAGAGTGGGGAAGCGGCTTCTGAGAGC	1091





OY	187	ProGlnTyrLeuSgLy---	GlyValHisCysTyrTyrHisGlySerIleArgGlyVal	205
Db	97	ACCCGACACACACCCGGCTGGAGACACCTCTACTACAGAGAACCTCCGGGGAAAC	156	
OY	206	LysASerSerLyValAlaLeuSerThrcCysAsnGlyLeuHisGlyMetPheGlyLysAsp	225	
Db	157	CCGACATCTTCGGCGCCCTCTCCACCTGGCAGGGGCTGTCATGGGGGTCTTCTCTATGG	216	
OY	226	ThrPheValTyrMetIleGluProLeuGluLeuVal-----HisAspGlyLysSerThr	243	
Db	217	AACTTAGCTTCACTCTGAGCCACCCAAAGAGGCTGGACCTTGGGAGACCCCTCAGGA	276	
OY	244	GlyArgProHisIleIleGlnLysThrLeuValGluGlnTyrSerLyGlnMetLysAsn	263	
Db	277	CCCTCTCCCACTATTTACCAGACCCC-TCCTCTCCAGATCCCTCCGGATG-----	329	
OY	264	LeuThrMetGluArgGlyAspGlnTrpPro-PheLeuSerGluGlnGlnTyrPheLys--	282	
Db	330	-----CAGGAACCCAGGCTGCTGTTCGTGCTGCTGCCCTGCAGTGGCTCTCC	377	
OY	283	-----ArgArgLyArgAlaValAsnProSerArgGly-----Ile	294	
Db	378	AAACCCGCCAGCTGAGAGAGAAAAGGACAGTCCG-----CGGGGACACCTACAGT	431	
OY	294	ePheGlnGluMetLyTyrLeuGlnGluMetIleValAsnAspHisIleTyrTyrLysLy	314	
Db	432	GCACAGTAAACCAAGATGTGGAGCTAATTGTGATCAACAGACACACACAGCTTTCGAGCA	491	
OY	314	SHisArgSerSerHisAlaHisThrAsnAsnPheAlaLysSerValValAsnLeuValAs	334	
Db	492	GATGGACAGTCCGGTGGCTCTCACACAGAACCTTTCCCAAGTCCCTGGCGAACCTTGCCGA	551	
OY	334	pSerIleTyrLysGlnGlnLeuAsnThrArgValValLeuValAlaValGlnThrTrpTh	354	
Db	552	TGTGATATACAGAGACAGCTCAACACTCGCATCTCTGGTGGCCAAGGAACATGGGC	611	
OY	354	rGlyLysAspGlnIleAspIleThrThrAsnProValGlnMetLeuHisGlnPheSerLy	374	
Db	612	AGATGGGACAAAGATCCAGTGCAGGATGACCTCTCGAGACACTGGACCCGAGTCATGAT	671	
OY	374	sTyrArgGlnArg---IleLysGlnHisAlaAspArgAlaValHisLeuIleSerArgValTh	393	
Db	672	CTTACGACGGAGAGGCTGGCTTGAGCCACAGTAACTCCACCCACTCTCTCGGGAGAGC	731	
OY	393	rPheHisTyrLysArgSerSerLeuSerTyrPheGlyGlyValCysSerArgThrArgG1	413	
Db	732	CTTCCAGAGCAGACAGACCGGGGAGCCTACGTGGGGGGGCATATGCTCTCTCTCCATGG	791	
OY	413	yValGlyValAsnGlnTyrGlyLeuProMetAlaValAlaGlnValLLeuSerGlnSerLe	433	
Db	792	CGGGGGTGTGAACGATGACGGCAACATGGGGGCGATGGCCGTGACCCCTGGCCCAACACT	851	
OY	433	uAlaGlnAsnLeuGlyIleGlnTrpTrp---GluProSerSerArgLysP---OlyCysAspCy	452	
Db	852	GGGACAGAACCTGGGACATGATGTGAAACAAACACCCGAGCTCGGACAGAGACTGCAAGTG	911	
OY	452	sThrGluSerTrpGlyCysIleMetGlnGlnThrLeuValSerHisSerArgLysPh	472	
Db	912	TCCAGACATCTCGGGCTGCTCATCTATGTAGAGAACCTGGTTCTCTACCTGCCCCCGAGT	971	
OY	472	eSerLysCysSerIleLeuGlnTyrArgAspPheLeuGlnArgGluGlnGlyAlaCysLe	492	
Db	972	CTCTCGCGTACACATCGACAGATGACACACAGTCTTTCGACAGAGGCTGTGACAGCTCT	1033	
OY	492	uPheAsnArgProThrLysLeuPheGluProThrGlnCysGlyAsnGlnTyrValGlnAl	512	
Db	1032	CTTCAACACAAAGCCCTCAAGCTCTCTGGACCCSSCAAGAGTGGGGAACGACTCTGTGAGAGC	1091	
OY	512	aGlyGlnGlnLysArgCysGlyPheHisValGlnCysTyr-----GlyLeuCysCys	529	
Db	1092	AGGGGAGGAGTGCACCTGGCTGGCTGCAGAGATGACAGCGGCGAGTGGACACTGGTGC	1151	

QY	529	slYslyScYssSerleuSerAsnGlyAlaHisGcYssSerAspGlyProCysAsnAsnTh	549
Db	1132	CAAGAATATGCACCCCTGACTCACAGACCCATGTGCAGCCAGCGGCTCTGCTGCCCC--	1205
QY	549	rSerCysLeuPheGlnProArgGlyTYrGluCysArGAspAlaValAsnGluCysAsp11	569
Db	1210	---TGCAGATACGAACAGCGGGGTGTGTGCTTGCCGAGAGCGGTAACAGACTGGACAT	1265
QY	569	eThrGluTYrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisLysGlnAspG1	589
Db	1266	CGGGAGACCTGCACCGGGGAGACTTCAGGCAGTCCCGGCTTAACCTGCACAACTGTGAGCG	1322
QY	589	YYrAlaCysAsnGlnAsnGlnGlyAlaArgCysThrAsnGlyLysCysLysThrArgAspAs	609
Db	1326	TTACTACTGTGTGCATGTAGACAGAGCGCGCTGCTACGAGAGTGCCTCAAAACCCGGGACCG	1386
QY	609	nGlnCysGlnTYrLLeTPrGlyThrLysAlaAlaGlySerAspLysPheCysTYrGluLys	629
Db	1386	GCAGTGCAGAGCTTTCTTTGGGGCCATAGCCGGCTCT-----GATCCCTTCTGCTACGAGAA	1433
QY	629	sLeuAsnThrGluGluTYrThrGluLysGlyAsnCysGlyLysAspGlyAspArGTrIlaG1	649
Db	1440	GCTGATGTGGAGGGGAGCGAGCGGGAGCTGTGGGCGCAAGGATCCGGCTGGGTCCA	1496
QY	649	nCysSerLysHisAspValPheCysGlyPheLeuLeuCysThrAsnLeuThrArgAlaPr	669
Db	1500	GTGCAGTAAAGCAGGACGAGCTGTGTGGCTCTCTCTGTGTGCACATCTGTGGAGCTCC	1556
QY	669	CArG1LeuGlnLeuGlnGlnGlyGluIleLeuProThrSerPheTYrHisGlnGlyArgVal	689
Db	1560	TGCGGTAGAGGACCTGGTGGGAGACATAGTAGTGCACCTTCTTCAACACAGGAGACGA	1616
QY	689	ILLeAspCysSerGlyAlaHisValValLeuAspAspArThrAspValGlyTYrValG1	709
Db	1620	GCTGGACATGCAGGGGAGGCGACACGTGCACCTGGCGGACCGCTGTACACTGAGCTATGTGA	1676
QY	709	uAspGlyThrProCysGlyProSerMetMetCysLeuAspArgLysCysLeuGlnIleG1	729
Db	1680	GGATGTGCACAGCTGTGGGGCCCTTAACATGTGTGGCTTGACATCTCCCTGCTCCACGCTTC	1733
QY	729	nAlaLeuAsnMetSerSerCysProLeuAspSerLysGlyLysValLysSerGlyHisG1	749
Db	1740	TGCTCTTCAACTTCACACCTGTGCCCCGGCAGTGGGAGCGCGGATTTGCTCCACACAGG	1796
QY	749	yValCysSerAsnGluAlaThrCysLLeCysAspPheThrTrpAlaGlyThrAspCysSe	769
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RESULT 8  
 US-08-484-355-7  
 : Sequence 7, Application US/08484355  
 : Patent No. 5705341  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: NAKAMURA, YUSUKE  
 :  
 : APPLICANT: EMI, MITSURU  
 :  
 : TITLE OF INVENTION: MDC PROTEINS AND DNAS  
 :  
 : TITLE OF INVENTION: ENCODING THE SAME  
 :  
 : NUMBER OF SEQUENCES: 20  
 :  
 : CORRESPONDENCE ADDRESS:  
 :  
 : ADDRESSEE: FLYNN, THELL, BOUTELL & TANIS P.C.  
 :  
 : STREET: 2026 Rambling Road

ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.  
STREET: 2026 Rambling Road

CITY: Kalamazoo  
STATE: Michigan  
COUNTRY: USA  
ZIP: 49008-1699  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage  
COMPUTER: IBM PC/XT/AT Compatible  
OPERATING SYSTEM: MS-DOS 5.0  
SOFTWARE: WordPerfect 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484.355  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/243,542  
FILING DATE: 13-MAY-1994  
APPLICATION NUMBER: JP 5-136602  
FILING DATE: 14 MAY 1993  
APPLICATION NUMBER: JP 5-257455  
FILING DATE: 22 SEPTEMBER 1993  
APPLICATION NUMBER: JP 6-49904  
FILING DATE: 23 FEBRUARY 1994  
APPLICATION NUMBER: JP 6-73328  
FILING DATE: 12 APRIL 1994  
APPLICATION NUMBER: JP 6-84470  
FILING DATE: 22 APRIL 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Terrence F. Chapman  
REGISTRATION NUMBER: 32 549  
REFERENCE/DOCKET NUMBER: Furuya Case 1313  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (616) 381-1156  
TELEFAX: (616) 381-5465  
INFORMATION FOR SEQ. ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2913 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
LIBRARY: human fetal brain cDNA library  
FEATURE:  
NAME/KEY: 5' UTR  
LOCATION: 1..27  
FEATURE:  
NAME/KEY: 3' UTR  
LOCATION: 2038..2913  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 28..2037  
US-08-484-355-7  
Alignment Scores:  
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Best Local Similarity: 53.25% Mismatches: 193  
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QY 206 LysAspSerLysValAlaLeuSerThrCysAsnGlyLeuHisGlyMetPheGluAspAsp 225  
DB 157 CCGACACTCTTGGCCGCTCTCCACCTGCGAGGGGTGATGGGCTTCTCTGATGGC 216  
QY 226 ThrPheValTyrMetIleGluProLeuGlnLeuVal-----HisAspGlnLysSerThr 243  
DB 217 AACTGACTTACATGTGGAGCCCAAGAGTGGCTGGACCTTGGGGAGCCCTCAGGGA 276  
QY 244 GlyArgProHisIleIleGlnLysThrLeuAlaGlyGlnTyrSerLysGlnMetLysAsn 263  
DB 277 CCCCTTCCCACTTATTACCGGACCC-TCTCTCCAGATCCCTCGGATG----- 329  
QY 264 LeuThrMetGluArgGlyAspGlnTyrPro-PheLeuSerGlnLeuGlnTyrPheLys-- 282  
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QY 283 -----ArgGlySerArgAlaValAsnProSerArgGly-----11 294  
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QY 294 ePheGlnGluMetLysTyrLeuGlnLeuMetIleValAsnAspHisLysThrTyrLysLys 314  
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QY 334 pSerIleTyrLysGlnLeuAsnThrArgValAlaValAlaValAlaGlnThrPrth 354  
DB 552 TGTGATATACAAAGACAGCTCAACACTGCATCGCTCGTGGTGAACATGGGCG 611  
QY 354 rGlnLysAspGlnIleAspIleThrAsnProValGlnMetLeuHisGlnPheSerLys 374  
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QY 374 sTyrArgGlnArg---IleLysGlnHisAlaAspAlaValHisLeuIleSerArgValTh 393  
DB 672 CTACCGAGGAGAGGCTGCTGCTGAGCCAGTAAATGACCACCACTCTTCTCGGGCAGAC 731  
QY 393 rPheHisTyrLysArgSerSerLeuSerTyrPheGlnGlyValLysSerArgThrArgL 413  
DB 732 CTTCACAGCAGCAGCAGCGGGGCGAGCTAGCTGGGGGAGCATATGCTCCCTGCCATGG 791  
QY 413 yValGlyValAsnGlnTyrGlyLeuProMetAlaValAlaGlnValLeuSerGlnSerIle 433  
DB 792 CGGGGCTGTGAACGAGTACGCAACATGCGGCGCATGGCCGTGACCTTGCAGAGCT 851  
QY 433 uAlaGlnAsnLeuGlyIleGlnTyr---GluProSerSerArgLysProLysCysAspCy 452  
DB 852 GCGACAGAACCTGGCATGATGTGGAAACAAACACCGGAGCTCGGAGGGAGCTCAAGTG 911  
QY 452 sThrGlnSerTyrPheGlyGlyCysIleMetGlnGlnTyrGlyValSerHisSerArgLysPh 472  
DB 912 TCCAGACATCTGCTGCGCTGCATCATGAGAGACACTGGTTTACCTGCCCCCAAGTT 971  
QY 472 eSerLysCysSerIleLeuGlnTyrArgAspPheLeuGlnArgGlyGlyGlyAlaCysLys 492  
DB 972 CTCTGCGTGAAGCATGACGAGTACCAACAGATTCTTCAGAGAGGTGGTGGACCTGCT 1031  
QY 492 uPheAsnArgProThrLysLeuPheGlnProThrGlnCysGlyAsnGlyTyrValGlnAl 512  
DB 1032 CTTCAACAGGCCCTTCAGCTCTGAGCCCAAGTGGGAGACGGCTTCGTGGAGGC 1091  
QY 512 aGlyGlnGlnCysAspCysGlyPheHisValGlnLysTyr-----GlyLeuCysCys 529  
DB 1092 AGGGAGGAGATCGACTGCGCTGCTGAGAGATGACACCCGCGAGGTGGCAACTGCTG 1151  
QY 529 sLysLysCysSerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnTh 549  
DB 1152 CAAGAAATGACCCCTGACTCAGACGCCATGTGACCGGCGGCTGCTGCTGCGCCGC-- 1209  
QY 549 rSerCysLeuPheGlnProArgGlyTyrGlnCysArgAspAlaValAsnGlnCysAsp11 569

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Db 1266 CCGGAGACCTGCACCCGGGAGCTTACCGACGTGCCCTTAACCTGGCAAGCTGGAGCG 1335
Oy 589 yTyraLcYasAnGlnAsnGlnGlyArgCysTyraSnglyGlnCysLysThrArgAspAs 609
Db 1326 TTACTACTGATGACATGAGAGGGCGCTGCTACGAGGTGGCGCMAAACCCGGAGCG 1385
Oy 609 nGlnCysGlnTyrLleTrpGlyThrLysAlaAlaGlySerAspLysPheCysTyrgL 629
Db 1386 GCAATGCCAGCTTCTTTGGGGCCATGCGGCTGCT-----GATCGCTTCTGCTACGAGAA 1439
Oy 629 sLeuAsnThrGlnGlyThrGlnLysGlyAsnGlyLysAspGlyLysAspGlyLysAla 649
Db 1440 GCTGAATGCTGAGGGAGGAGCGAGCTGGAGACTGTGGGCGCAGAGGATCCGGCTGGTCA 1499
Oy 649 nCysSerLysHisAspValPheCysGlyPheLeuLeuCysThrAsnLeuThrArgAla 669
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Oy 669 oArgLleGlyGlnLeuGlnGlyGlnLleLeuProThrSerPheTyrHISglnGlyArg 689
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Oy 709 uAspGlyThrProCysGlyProSerMetCysLeuAspArgLysCysLeuGlnLleG 729
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Oy 788 oSerAlaThrAsnLeuLleLleGlySerLleAlaGlyAlaLleLeuValAlaLleVal 808
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Oy 808 lLeuGlyGlyThrGlyTyrPglYrPheLysAsnValLysLysArgArg 823
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RESULT 9
US-08-243-542-6
: Sequence 6, Application US/08243542
: Patent No. 5552526
: GENERAL INFORMATION:
: APPLICANT: NAKAMURA, YUSUKE
: TITLE OF INVENTION: EMT, MITSURU
: TITLE OF INVENTION: MDC PROTEINS AND DNAs
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P. C.
: STREET: 2026 Rambling Road
: CITY: Kalamazoo
: STATE: Michigan
: COUNTRY: USA
: ZIP: 49008-1699
: COMPUTER READABLE FORM:
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: MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
: COMPUTER: IBM PC/XT/AT Compatible
: OPERATING SYSTEM: MS-DOS 5.0
: SOFTWARE: WordPerfect 5.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/243,542
: FILING DATE:
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 5-136602
: FILING DATE: 14 MAY 1993
: APPLICATION NUMBER: JP 5-257455
: FILING DATE: 22 SEPTEMBER 1993
: APPLICATION NUMBER: JP 6-49904
: FILING DATE: 23 FEBRUARY 1994
: APPLICATION NUMBER: JP 6-73328
: FILING DATE: 12 APRIL 1994
: APPLICATION NUMBER: JP 6-84470
: FILING DATE: 22 APRIL 1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Terrence F. Chapman
: REGISTRATION NUMBER: 32 549
: REFERENCE/DOCKET NUMBER: Furuya Case 1313
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (616) 381-1156
: TELEFAX: (616) 381-5465
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2923 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: IMMEDIATE SOURCE:
: LIBRARY: human fetal brain cDNA library
: FEATURE:
: NAME/KEY: 5' UTR
: LOCATION: 1..27
: FEATURE:
: NAME/KEY: 3' UTR
: LOCATION: 1600..2923
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 28..1599
: US-08-243-542-6
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: Best Local Similarity: 53.09% Mismatches: 192
: Query Match: 40.48% Indels: 37
: DB: 1 Gaps: 14
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Db 37 CTGAGCCACCAACATCTCTCTCGCAATACCTGAGCGCCACTTCACCCGGAGGAGCA 96
Oy 187 ProGlnTyrSerLysGly---GlyGlnHisCysTyrTyrHisGlySerLleArgGlyVal 205
Db 97 ACCCAGACAGACACCGGGGCTGGAGACCACTGCTACTACCAAGGAGAGCTCCGGGAGAC 156
Oy 206 LysAspSerLysValAlaLeuSerThrCysAsnGlyLeuHisGlyMetPheGluAspAsp 225
Db 157 CCGCACTCCTTCCGGCGGCTCTCCACCTCCAGGGGCTGCATGGGCTTCTCTGATGGG 216
Oy 226 ThrPheValIyrMetLleGluProLeuGlnLeuVal-----HisAspGlyLysSerThr 243
Db 217 AACTTGAATTACATCGTGAAGACCCCAAGAGGTGGCTGACCTTGGAGAGCCCTCAAGGA 276
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus.p2n model

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(without alignments)  
3714.701 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5  
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Searched: 845702 seqs, 674182571 residues

Total number of hits satisfying chosen parameters: 1691404

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	4553	100.0	4043	10	US-09-824-129-2	Sequence 2, Appli
2	3621	79.5	2268	10	US-09-809-790-1	Sequence 1, Appli
3	3621	79.5	2268	10	US-09-809-617-1	Sequence 1, Appli
4	3007	66.0	2088	10	US-09-809-790-3	Sequence 3, Appli

5	3007	66.0	2088	10	US-09-809-617-3	Sequence 3, Appli
6	1680	36.9	1668	10	US-09-792-200B-17	Sequence 17, Appli
7	1029.5	22.6	3512	9	US-10-020-733-9	Sequence 9, Appli
8	1016.5	22.3	6488	9	US-10-161-803-48	Sequence 48, Appli
9	1012.5	22.2	6475	9	US-10-161-803-49	Sequence 49, Appli
10	1007.5	22.1	2757	9	US-10-020-733-3	Sequence 3, Appli
11	1007.5	22.1	2757	9	US-10-125-470-2	Sequence 2, Appli
12	1007.5	22.1	2757	9	US-10-125-452-2	Sequence 2, Appli
13	1007.5	22.1	2757	9	US-09-955-504-2	Sequence 2, Appli
14	1007.5	22.1	2781	9	US-10-020-733-1	Sequence 1, Appli
15	1007.5	22.1	2868	9	US-10-020-733-7	Sequence 7, Appli
16	1007.5	22.1	2892	9	US-10-020-733-5	Sequence 5, Appli
17	982	21.6	1674	10	US-09-792-200B-15	Sequence 15, Appli
18	981	21.5	7920	12	US-10-044-090-781	Sequence 781, App
19	978	21.5	6352	10	US-09-983-531A-3	Sequence 3, Appli
20	977.5	21.5	3305	9	US-09-978-295A-73	Sequence 73, Appli
21	977.5	21.5	3305	9	US-09-978-667-73	Sequence 73, Appli
22	977.5	21.5	3305	9	US-09-978-192A-73	Sequence 73, Appli
23	977.5	21.5	3305	9	US-09-999-832A-73	Sequence 73, Appli
24	977.5	21.5	3305	9	US-09-978-189-73	Sequence 73, Appli
25	977.5	21.5	3305	9	US-10-174-590-87	Sequence 87, Appli
26	977.5	21.5	3305	9	US-10-176-758-87	Sequence 87, Appli
27	977.5	21.5	3305	9	US-10-175-737-87	Sequence 87, Appli
28	977.5	21.5	3305	9	US-10-173-706-87	Sequence 87, Appli
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31	977.5	21.5	3305	9	US-10-176-482-87	Sequence 87, Appli
32	977.5	21.5	3305	9	US-10-176-757-87	Sequence 87, Appli
33	977.5	21.5	3305	9	US-10-176-913-87	Sequence 87, Appli
34	977.5	21.5	3305	9	US-10-180-552-87	Sequence 87, Appli
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37	977.5	21.5	3305	9	US-10-174-572-87	Sequence 87, Appli
38	977.5	21.5	3305	9	US-10-174-579-87	Sequence 87, Appli
39	977.5	21.5	3305	9	US-10-174-582-87	Sequence 87, Appli
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43	977.5	21.5	3305	9	US-10-175-743-87	Sequence 87, Appli
44	977.5	21.5	3305	9	US-10-176-488-87	Sequence 87, Appli
45	977.5	21.5	3305	9	US-10-176-492-87	Sequence 87, Appli

ALIGNMENTS

RESULT 1  
US-09-824-129-2  
Sequence 2, Application US/09824129  
Patent No. US20020001840A1  
GENERAL INFORMATION:  
APPLICANT: Lopez-Otin, Carlos  
APPLICANT: Miguell, Santiago Cal  
APPLICANT: Freije, Jose Maria Perez  
APPLICANT: Garcia, Jose Manuel Lopez  
APPLICANT: Bianchi, Albert Bernard  
APPLICANT: Trail, Pamela  
TITLE OF INVENTION: Methods and Compositions for Modulating  
Integrin-mediated Cell-Cell Interactions  
FILE REFERENCE: D0015-NP  
CURRENT APPLICATION NUMBER: US/09/824,129  
CURRENT FILING DATE: 2001-04-02  
PRIOR APPLICATION NUMBER: 60/194,164  
PRIOR FILING DATE: 2000-04-03  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 4043  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-824-129-2  
Alignment Scores: 0  
Pred. No.: 0  
Length: 4043

Score: 4553.00 Matches: 832  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Gaps: 0  
DB: 10

US-09-634-252a-4 (1-832) x US-09-824-129-2 (1-4043)

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QY 21 AlaSerGlyProGlyArgGlyProAlaGlySerValProAlaSerAlaProAlaArg 40  
Db 1077 GCTTCTCGCGCGCGCGCGCGCGCGCGCGCGCTGGGCTGCGCAGCGCGCGCGCGC 1136  
QY 41 ThrProCysArgLeuLeuLeuValLeuLeuLeuLeuProProLeuAlaAlaSerSer 60  
Db 1137 AGCGCGCGCTGCGCGCTGCTCTGCTCTCTGCTCTGCTCTGCTCTGCTCTGCTCT 1196  
QY 61 ArgProAlaGlyArgGlyValAlaAlaAlaProSerAlaProHisThrPasnGluThrAlaGlu 80  
Db 1197 CGCGCGCGCGCTGGGGGCTGCTGCGCGCGCGCTGCGCGCGCTGCGCGCGCTGCG 1256  
QY 81 LysAsnLeuGlyValLeuAlaAspGluAspAsnThrLeuGlnGlnAsnSerSerAsn 100  
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QY 101 LLeSerTyrSerAsnAlaMetGlnLysGluLLeThrLeuProSerArgLeuLLeTyr 120  
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QY 121 LLeAsnGluAspSerLysSerProTyrHisValLeuAspThrLysAlaArgHisGln 140  
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QY 141 LysHisAsnLysAlaValHisLeuAlaGlnAlaSerPheGlnLLeGluAlaPheGlySer 160  
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QY 161 LysPheLLeLeuAspLeuLLeLeuAsnAsnGlyLeuLeuSerSerArgValAlaGluLLe 180  
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QY 221 MetPheGluAspAspThrPheValTyrMetLLeGluProLeuGluLLeuValHisAspGlu 240  
Db 1677 ATGTTTCAAAATGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1736  
QY 241 LysSerThrGlyArgProHisLLeLLeGlnLysThrLeuAlaGlyGlnTyrSerLysGln 260  
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QY 281 LeuLysArgArgLysArgAlaValAsnProSerArgLLePheGlnGluMetLysTyr 300  
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QY 301 LeuGluLeuMetLLeValAsnAspHisLysThrTyrLysLysHisArgSerSerHisAla 320  
Db 1917 TTGGAACTTATGATGTTATATGATCACAAGAGTAAAGAGAGAGAGAGAGAGAG 1976  
QY 321 HisThrAsnAsnPheAlaLysSerValValAsnLeuValAspSerLLeTyrLysGluGln 340

Db 1977 CATACCAACCACTTGCAGAAATCCGCTGCTCAACTCTTGATTCATTTACAAAGACAG 2036  
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QY 361 LLeThrThrAsnProValGlnMetLeuHisGluPheSerLysTyrArgGluArgLLeLys 380  
Db 2097 ATCAACCAACCACTTGCAGAGTGCATGATGATTTCAAAATACCGCAGCGCATTTAG 2156  
QY 381 GlnHisAlaAspAlaValHisLeuLLeSerArgValLLePheHisTyrLysArgSerSer 400  
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QY 401 LeuSerTyrPheGlyLysValCysSerArgThrArgGlyValGlyValAsnGluTyrGly 420  
Db 2217 CTGAGTTACTTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2276  
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Db 2277 CTTCCAATGCGAGTGGCACAGATATTATGCGAGAGCTGGCTCAAAACCTTGGAA 2336  
QY 441 TrrGluProSerSerArgLysProLysCysAspCysThrGluSerTrpGlyLysCys 460  
Db 2337 TGGAGACCTTTCTACAGAAAGCCAAATGCTGACTGACAGAAATCCGGGCTGCTG 2396  
QY 461 MetGluGluThrGlyValSerHisSerArgLysPheSerLysCysSerLLeuGluTyr 480  
Db 2397 ATGAGAGAAACAGGGGTGCCATTTCTCGAAATTTTCAAGAGCGAGCATTTTGGAG 2456  
QY 481 ArgAspPheLeuGlnArgGlyGlyValAlaCysLeuPheAsnArgProThrLysLeuPhe 500  
Db 2457 AGAGACTTTTACAG 2516  
QY 501 GluProThrGluCysGlyAsnGlyTyrValGluAlaGlyLysLysAspCysGlyPhe 520  
Db 2517 GAGCCACGGAATCTGGAATGATGATGATGATGATGATGATGATGATGATGATG 2576  
QY 521 HisValGluCysTyrGlyLeuCysCysLysLysCysSerLeuSerAsnGlyAlaHisCys 540  
Db 2577 CATGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2636  
QY 541 SerAspGlyProCysAsnAsnThrSerCysLeuPheGlnProArgGlyTyrGluCys 560  
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QY 561 ArgAspAlaValAsnGluCysAspLLeThrGluTyrCysThrGlyAspSerGlyLys 580  
Db 2697 CGGATCTGTAAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2756  
QY 581 ProProAsnLeuHisLysGlnAspGlyTyrAlaCysAsnGlnAsnGlnLysArgCysTyr 600  
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QY 601 AsnGlyLysCysLysThrArgAspAsnGlnCysGlnTyrLLeTrrPglTyrHisAlaAla 620  
Db 2817 AATGGCAGAGTCAAGACAGAGACAGAGACAGAGTCAATCAATCAATCAATCAAT 2876  
QY 621 GlySerAspLysPheCysTyrGluLysLeuAsnThrGluGlyThrGluLysGlyAsnCys 640  
Db 2877 GGGTCTGCAAGTCTGCTGATGAAAGCTGATGAAAGCTGATGAAAGCTGATGAAAG 2936  
QY 641 GlyLysAspGlyAspArgTrpLLeGlnCysSerLysHisAspValPheCysGlyPheLeu 660  
Db 2937 GGAAGAGATGAG 2996  
QY 661 LeuCysThrAsnLeuThrArgAlaProArgLLeGlyGlnLeuGlnGlyLLeLLePro 680  
Db 2997 CTCTGTACCAATCTTACTGAGCTCAGCTGATGATGATGATGATGATGATGATGAT 3056  
QY 681 ThrSerPheTyrHisGlnGlyArgValLLeAspCysSerGlyAlaHisValValLeuAsp 700



Dh 3057 ACTTCCTTCTACCATCAGAGCCGGGTGATTGACTGCAGTGGTCCCATGTAGTTTATAGAT 3116  
Oy AspAspThrAspValGlyTyrValGluAspGlyThrProCysGlyProSerMetMetCys 720  
Dh 3117 GATGATACGGATGTGGCTATGTAGAGATGAGAACCCCATGTGGCCGCTATGATGTGT 3176  
Oy LeuAspArgLysCysLeuGlnIleGlnAlaLeuAsnMetSerSerCysProLeuAspSer 740  
Dh 3177 TTAGATCGGAGAGGCTTACAAATTCAGGCCCTAAATATGAGACGCTGTCCACATTC 3236  
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Dh 3237 AAGGGTAAGTCTGTTGGGGCCATGGGGTGTAGTAATCAAGCCCATCTGCATTTGTGAT 3296  
Oy PheThrTriPalaGlyThrAspCysSerIleArgAspProValIArgAsnLeuHisProPro 780  
Dh 3297 TTCACCTGGGACAGGACAGATTCACATTCGGGATTCACATTAGAACCTTCACCCCC 3356  
Oy LysAspGluGlyProLysGlyProSerAlaThrAsnLeuIleIleGlySerIleAlaGly 800  
Dh 3357 AAGATGAGAGAGACCAAGGGTCTTACAGCCCAATCTCATATAGGCTCATCGGTGT 3416  
Oy AlaIleLeuValAlaIleValIleValIleGlyGlyThrGlyTyrProGlyPheLysAsnValLys 820  
Dh 3417 GCCATCTCGTACACCTATTTGCTTGGGGCAGAGCGGTGAAATTAATATGTCAG 3476  
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RESULT 2  
US-09-809-790-1  
Sequence 1, Application US/09809790  
Patent No. US20020072102A1  
GENERAL INFORMATION:  
APPLICANT: Sheppard, Paul O.  
APPLICANT: Balindur, Nand  
APPLICANT: Delisher, Theresa A.  
APPLICANT: Bishop, Paul D.  
TITLE OF INVENTION: DISINTEGRIN HOMOLOG  
FILE REFERENCE: 98-29  
CURRENT APPLICATION NUMBER: US/09/809,790  
CURRENT FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 09/351,414  
PRIOR FILING DATE: 1999-07-09  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 2268  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (3)...(2090)  
NAME/KEY: misc.feature  
LOCATION: (1)...(2268)  
OTHER INFORMATION: n = A,T,C or G  
US-09-809-790-1

Alignment Scores:  
Pred. No.: 0 Length: 2268  
Score: 3621.00 Matches: 654  
Percent Similarity: 99.70% Conservative: 0  
Best Local Similarity: 99.70% Mismatches: 2  
Query Match: 79.53% Indels: 0  
DB: 10 Gaps: 0

US-09-634-252a-4 (1-832) x US-09-809-790-1 (1-2268)

Oy 132 LeuAspThrLysAlaArgHisGlnGlnLysHisAsnLysAlaValHisLeuAlaGlnAla 151  
Dh 27 CTTGACACAAAGGCAAGACACACGACAAACATATATAGGCTGTCCATCTGGCCACGAGCA 86

Oy 152 SerPheGlnIleGlnAlaPheGlySerLysPheIleLeuAspLeuIleLeuAsnGly 171  
Dh 87 AGCTTCAGATTGAAGCTTCGGCTCCCAATTCATCTTGCACCATATGACCAATGCT 146  
Oy 172 LeuLeuSerSerAspTyrValGluIleHisTyrGluAsnGlyLysProGlnTyrSerLys 191  
Dh 147 TTCTTGCTCTCTGATTAATGAGAGATTCACTAGCAAAATGCGAAACACAGTACTTAAG 206  
Oy 192 GlyGlyGlnHisCysTyrTyrHisGlySerIleArgGlyValLysAspSerLysValAla 211  
Dh 207 GGTGGAGACAGCTGTACTACCATGGAAGCATCAGAGGCTCAAGACTCCAAAGGTGGCT 266  
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Dh 267 CTGTCAACCTGCATGAGCATCTTCATGGCATGTTGAAGATGATACCTCGTATATGATA 326  
Oy 232 GluProLeuGlnLeuValHisAspGlyLysSerThrGlyArgProHisIleIleGlnLys 251  
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Oy 252 ThrLeuAlaGlyIleTyrSerLysGlnMetLysAsnLeuThrMetGluArgGlyAspGln 271  
Dh 387 ACCTTGGCAGACAGATATTCTTAAGCAATAGACATCTCATGGAAGAGGTGACAG 446  
Oy 272 TrpProPheLeuSerGlyLeuGlnIleTrpLeuLysArgArgLysArgAlaValAsnProSer 291  
Dh 447 TGGCCCTTCTCTCTGATTAACAGTGGTGAAGAAAGAGAGAGAGATGATTCATCA 506  
Oy 292 ArgGlyIlePheGlyGluMetLysTyrLeuGlnLeuMetIleValAsnAspHisLysThr 311  
Dh 507 CGTGTATATTTGAAGAAATGAATATTTGCACTTGTGATTTGATATGATCAACAAAG 566  
Oy 312 TyrLysLysHisArgSerSerHisAlaHisThrAsnAsnPheAlaLysSerValAsn 331  
Dh 567 TATTAAGAGCATGCGCTTCTTCATGCACATACCAACACTTTTGAAGATCCGTGTCAAC 626  
Oy 332 LeuValAspSerIleTyrLysGlnGlnLeuAsnThrArgValAlaLeuValAlaValGlu 351  
Dh 627 CTGTGGATTTCTATTATTAAGAGAGACAGCTCAACAGCGGGTTCGTGGGTGTAGAG 686  
Oy 352 ThrTrpThrLysAspGlnIleAspIleThrThrAsnProValGlnMetLeuHisGly 371  
Dh 687 ACCTGACCTGAGAGGATGAGATTGACATCACCCCAACCTGTGCAGATGCTCCAGAG 746  
Oy 372 PheSerLysTyrArgGlnArgIleLysGlnHisAlaAspAlaValHisLeuIleSerArg 391  
Dh 747 TTCTCAAAATACCGGAGCGCATTAAGCAGCATGCTGATGCTGTGCACCTCATCTCCGG 806  
Oy 392 ValThrPheHisTyrLysArgSerSerLeuSerTyrPheGlyGlyValCysSerArgThr 411  
Dh 807 GTGACATTTCACTATATAGAGAGACAGCTGAGTTACTTTGAAGGTGTCGTTCGCGACA 866  
Oy 412 ArgGlyValGlyValAsnGlyTyrGlyLeuProMetAlaValAlaGlnValLeuSerGln 431  
Dh 867 AGAGAGCTGTGCTGAAATGAGTATGCTTCCATGACAGTGCAGCAAGATTAATCCAG 926  
Oy 432 SerLeuAlaGlnAsnLeuGlyIleGlnTrpGlnProSerSerArgLysProLysCysAsp 451  
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Oy 472 PheSerLysCysSerIleLeuGlyTyrArgAspPheLeuGlnArgGlyGlyAlaCys 491  
Dh 1047 TTTTCAAAAGTCAAGCATTTTGAATATGAGACTTTTACAGAGAGAGGTGACCTGC 1106  
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Dh 1107 CTTTTCACAGGCGCAACAGACTATTTGAGCCCGGAAATGTGAAATGATACGTGAA 1166  
Oy 512 AlaGlyGlnGlyCysAspCysGlyPheHisValGlnCysTyrGlyLeuCysCysLysLys 531

b	1167	CGTGGGAGAGTGTGATTGTGGTTTATGTGGAATGCTATGCAATTATGGCTGAAGAA	1226
y	532	CysSerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCys	551
b	1227	TGTTCCCTCTCCACACGGGGCTCAGTCGACGACGACGGGCCCTGGCTGAACAATACCCATGT	1286
y	552	LeuPheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGlu	571
b	1287	CTTTTTCACCCACGAGAGGTATGAATGCCGGGATGGCTGTGAACAGAACTGTGATTAATCTAA	1346
y	572	TyrCysThrGlyAspSerGlyGlnCysProPheAsnLeuHisGlnAspGlyTyrAla	591
b	1347	TATTGTACTGGAACTCTGGTCAGTCCACCAATCTTCATTAAGCAAGACGATATGCA	1406
y	592	CysAsnGlnAsnGlnGlyArgCysTyrAsnGlyGluCysLysLysThrArgAspAsnGlnCys	611
b	1407	TGCAATCAAAATCAGGGGCCGCTCTACAAATGGCGAATGCCAAGACGAAACCAACGATGT	1466
y	612	GlnTyrIleThrPheGlyThrLysAlaAlaGlySerAspLysPheCysTyrGluLysLeuAsn	631
b	1467	CAGTACACTCTGGGGAACAAAGCGGTGAGAGGTCTGCAACAGCTTCTGCTATATAAAGCTCAAT	1522
y	632	ThrGlnGlyThrGluLysGlyAsnCysGlyLysAspGlyAspArgTyrIleGlnCysSer	651
b	1527	ACAAAGGCACTGGAAGGGAACCTGCGGGAAGATGGAACCCGGATTCAGTCACTCAC	1588
y	652	LysHisAspValPheCysGlyPheLeuLeuCysThrAsnLeuThrArgAlaProArgIle	671
b	1587	AAACATGATGTTGTTCTGTGGATTCCTTACTCTGTAACCAATCTTACTGAGCTCCACGATTT	1644
y	672	GlyGlnLeuGlnGlyGluIleIleProThrSerPheTyrHisGlnGlyArgValIleAsp	691
b	1647	GGTCAACTTCAGGGGTGAGATCATTCCAAATCTCTTACCATCAAGGCCGGGAGATTGAC	1704
y	692	CysSerGlyAlaHisValIleAspAspAspThrAspValGlyTyrValGluAspGly	711
b	1707	TGCAGTGGTGGCCCATGTGATTGTTAGATGATCATCGGATGTGGGCTATGTAGAAGATGGA	1766
y	712	ThrProCysGlyProSerMetMetCysLeuAspArgLysCysLeuGlnIleGlnAlaLeu	731
b	1767	ACGCCATGTGGCCGCTATGATGTGTTAAGTCGGAAGTGCCCTACAAATTCACAGCCCTA	1822
y	732	AsnMetSerSerCysProLeuAspSerLysGlyLysValCysSerGlyHisGlyValCys	751
b	1827	AATAGACACAGCTGCACCTCGATTCCAAAGGTAAAGTCTGTTGGGCCCATGGGGTGTGT	1888
y	752	SerAsnGluAlaThrCysIleCysAspPheThrTrpAlaGlyThrAspCysSerIleArg	771
b	1887	AGTAAATGAAGCACCTGCATTTGTGATTTCAACCTGGCAGGACAGATTGCAGTATCCGG	1944
y	772	AspProValArgAsnLeuHisProProLysAspGluGlyProLysGly	787
b	1947	GATCCAGTTAGGAACCTTCACCCCCCAAGATGAAGACCCAAAGGT	1994
RESULT 3			
US-09-809-617-1			
: Sequence 1, Application US/09809617			
: Patent No. US20020137178A1			
GENERAL INFORMATION:			
APPLICANT: Sheppard, Paul O.			
APPLICANT: Bainsdur, Nand			
APPLICANT: Delisher, Theresa A.			
APPLICANT: Bishop, Paul D.			
TITLE OF INVENTION: DISINTEGRIN HOMOLOG			
FILE REFERENCE: 98-29			
CURRENT APPLICATION NUMBER: US/09/809,617			
CURRENT FILING DATE: 2001-03-15			
PRIOR APPLICATION NUMBER: US/09/351,414			
PRIOR FILING DATE: 1999-07-09			
NUMBER OF SEQ ID NOS: 13			
SOFTWARE: FastSeq for Windows Version 3.0			
: SEQ ID NO 1			

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?      LENGTH: 2268
?      TYPE: DNA
?      ORGANISM: Homo sapiens
?      FEATURE:
?      NAME/KEY: CDS
?      LOCATION: (3)..(2090)
?      NAME/KEY: misc_feature
?      LOCATION: (1)..(2268)
?      OTHER INFORMATION: n = A,T,C or G
?
US-09-809-617-1

Alignment Scores:
Pred. No.:
Score: 0
Percent Similarity: 3621.00
Best local Similarity: 99.70%
Query Match: 79.53%
DB: 10

Length: 2268
Matches: 654
Conservative: 2
Mismatch: 0
Indels: 0
Gaps: 0

US-09-634-252A-4 (1-832) x US-09-809-617-1 (1-2268)

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QY	152	SerPheGlnIleGlnIleAlaPheGlySerLysPheIleLeuAspLeuIleLeuAsnAsnGly	171
Db	87	AGCTTCCAGATTTGAAGCCCTTCGGCTCCAAATTCATTCTTGACCTCATACTGAACAATGGT	146
QY	172	LeuLeuSerSerAspTyrValGlnIleHisTyrGlnAsnGlyLysProGlnTyrSerLys	191
Db	147	TTGTTGTCTTCTGATTATGTGGAGATTCACTACGAATAATGGAAACCACACTACTCTAAG	206
QY	192	GlyGlyGlnHisCysTyrTyrHisGlySerIleArgGlyValLysAspSerLysValAla	211
Db	207	GGTGAGAGACACTGTTACTACCATGAAGCAACAGGCGCTCAAGACTCCAAAGTGGCT	266
QY	212	LeuSerThrCysAsnGlyLeuHisGlyMetPheGlnAspPheThrPheValTyrMetIle	231
Db	267	CTGTCAACCTGGCAATGGACTTCATGGCATGTTGAAGATGATACCTTGCTGATATGCATA	326
QY	232	GluProLeuGlnLeuValHisAspGlyLysSerThrGlyArgProHisIleIleGlnLys	251
Db	327	GAGCCACTGAGACTGGTTCATGATGAGAAACACAGGCGCACCATATATATCCAGAA	386
QY	252	ThrLeuAlaGlyGlnTyrSerLysGlnMetLysAsnLeuThrMetGlnArgGlyAsnGln	271
Db	387	ACCTTGGCAGGACAGATTTCTAAGCAATGAAGAACTCTACATGTGAAGAGGTGCACAG	446
QY	272	TrpProPheLeuSerGlnLeuGlnIleProLeuLysArgArgLysArgAlaValAsnProSer	291
Db	447	TGGCCCTTTCTCTCAATTTACAGTGCGTTGAAGAAGAGAGGACACTGATCCATTA	506
QY	292	ArgGlyIlePheGlnGlnMetLysTyrLeuGlnLeuMetIleValAsnAspHisLysThr	311
Db	507	CGTGGAATATATTGAAGAAATGAATATTGGAACTTATGTTGGTAATGATCCAAACAG	566
QY	312	TyrLysLysHisArgSerSerHisAlaHisThrAsnAspPheAlaLysSerValValAsn	331
Db	567	TATPAGAGAGATGCCTCTTCTCATGCACATACCAACAACCTTGCAAAGTCCGGGTCAAC	626
QY	332	LeuValAspSerIleTyrLysGlnGlnLeuAsnThrArgValValLeuValAlaValGln	351
Db	627	CTTGTGGATTCTATTATTCAGAAGGACACTCAACACCGGCTTGCTCGGTGGCTGTAGAG	686
QY	352	ThrTrpThrGlyLysAspGlnIleAspIleThrThrAsnProValGlnMetLeuHisGln	371
Db	687	ACCTGCACTGGAAGGATGACATTTGACATCAACCCAAACCTGTGCAGATGCTCCATGAG	746
QY	372	PheSerLysTyrArgGlnArgIleLysGlnHisAlaAspAlaValHisLeuIleSerArg	391
Db	747	TTTCATAAATATACCGGACGCGCATTTAACCAGCATCTGATGTGTGCACATCATCTCCGG	806



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Db      388 YTNCGNGNCARATWASNAARCARATGAAARAATTNACNATGGAGMGNGCAATCARTGG 447
Oy      273 ProPheLeuSerGluLeuGlnTrpLeuLysArgArgAlaValAsnProSerArg 292
Db      448 CCNTTYTNMSGAVTYTCARTGTYTNAARMGNCNMGNCNGTNAAYCCNMSNMGN 507
Oy      293 GlyIlePheGluGluMetLysTrpLeuGluMetIleValAsnAspHisLysThrTrp 312
Db      508 GGNATHHTTGARGARATGAAATTAAYTNGARNTNATGATGNGNAAGCAVCAARACNTAY 567
Oy      313 LysLysHisArgSerSerHisAlaHisThrAsnAsnPheAlaLysSerValValAsnLeu 332
Db      568 AARAAKCAIWMGWSMWSNCAYGCNCAACNAAYTAATTYGCNAARMSNTNCTNNAAYTN 627
Oy      333 ValAspSerIleTrpLysGluGlnLeuAsnThrArgValValLeuValAlaValGluThr 352
Db      628 GNGAGWASNAHTDAVAARCARATNAAYACNMGNGTNGTNTNCTNCGNGTNGNARCN 687
Oy      353 TrpThrGluLysAspGlnIleAspIleThrThrAsnProValGlnMetLeuHisGluPhe 372
Db      688 TGGACNGAARARCAATCAATGATGATACNACNAAYCCNGTNCARATGTYTNCAYGARTTY 747
Oy      373 SerLysTrpArgGlnArgIleLysGlnHisAlaAspAlaValHisLeuIleSerArgVal 392
Db      748 WSNAAATATMGNCARMGNTHAARCARCAVCGNGAYCGNGTNCAYTNTATWMSMGNGTN 807
Oy      393 ThrPheHisTrpLysArgSerSerLeuSerTrpPheGlyGlyValAlaCysSerArgThrArg 412
Db      808 ACNTTYCAVTAAYAAARMGWSMWSMNTNMTATYTTGARGNGTNGTNGWSMNGNACMGN 867
Oy      413 GlyValGlyValAsnGluTrpGlyLeuProMetAlaValAlaGlnValIleSerGlnSer 432
Db      868 GGNCTGNGTNAAYGARTYAGGTYTNCNATGGCNGTNCNCARNTNNTNMSNCAWMSN 927
Oy      433 LeuAlaGlnAsnLeuGlyIleGlnTrpGluProSerSerArgLysProLysCysAspCys 452
Db      928 YTNCGNCARAAAYTNGNATHCARATGGAGCCNMSNMNGNAAARCCNAARTGAYTGY 987
Oy      453 ThrGluSerTrpGlyLysIleMetGluGluThrGlyLysSerHisSerArgLysPhe 472
Db      988 ACNGARMSNTGGGNGGNGTGYATGATGARGARACNGNGTNGNCAWWSMNGNAARTTY 1047
Oy      473 SerLysCysSerIleLeuGluTrpArgAspPheGlnArgGlnArgGlyGlyAlaCysLeu 492
Db      1048 WSNAAARGYSNATHYTNGATTAAGCATYTTTNCARMGNGGNGGNGGNGTGYTNT 1107
Oy      493 PheAsnArgProThrLysLeuPheGluProThrGluCysGlyAsnGlyTrpValGluAla 512
Db      1108 TTYAAYMGNCNACNAARAYTNTTYGARCNCNCGARTGYGNAAYGGNTAYGTNGARCN 1167
Oy      513 GlyGluLysCysAspCysGlyPheHisValGluCysTrpGlyLeuGlyCysLysLysCys 532
Db      1168 GGNARGARFTGYGATGGTTCAYCTNGARTGYTAYGGNTYNTGTYGAARARARGY 1227
Oy      533 SerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnAspThrSerCysLeu 552
Db      1228 WSNYTNMSNAAYGGNGCARTTGYMSNCAATGNCNCNTGYTGAATAAACMSNNTGYTNT 1287
Oy      553 PheGlnProArgGlyTrpGluCysArgAspAlaValAsnGluCysAspIleThrGluTrp 572
Db      1288 TTYCARGCNCMNGGNTAYGARTGYGNGAYGNGTNAAYGARTGYGAVATHACNARAY 1347
Oy      573 CysThrGlyAspSerGlyGlnCysProProAsnLeuHisLysGlnAspGlyTrpTrpLacys 592
Db      1348 TGYACNGNGAGAWMSGNCARTGYCCNCAAYTNCAYAAARCAAGAVGGNTAYGCTGY 1407
Oy      593 AsnGlnAsnGlnGlyArgCysTrpAsnGlyGluCysLysThrArgAspAsnGlnCysGln 612
Db      1408 AAYCAARAAYCARGMNGNTGYTAAYAAVNGARGTGAARACMNGCAVAAAYARCTGYCAR 1467
Oy      613 TyrIleTrpGlyThrLysAlaAlaGlySerAspLysPheCysTrpGlyLysLeuAsnThr 632

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Db      1468 TAYATHTGGGNACNAARCGNCGNMSNCAVAAARTTYTGTAYAGARARTNNAAYCN 1527
Oy      633 GlnGlyThrGluLysGlyAsnCysGlyLysAspGlyAspArgTrpIleGlnCysSerLys 652
Db      1528 GARGNACNGAARAAAGNAATYGTGCGNARAGAYGNGAYGNGTGTATCARGYWSNAR 1587
Oy      653 HisAspValPheCysGlyPheLeuLeuCysThrAsnLeuThrArgAlaProArgIleGly 672
Db      1588 CAYGAVGTNTTYTGYGNGTYYTNTNTGYACNAAAYTNACMNGMNGCNCNMGNTHTGN 1647
Oy      673 GlnLeuGlnGlyGlnIleLeuProThrSerPheTrpHisGlnGlyArgValIleAspCys 692
Db      1648 CARNTNACARGNGARTRTHATGCCNACMSNTTYTAYCAICARGMNGNNTNTHAGTYCY 1707
Oy      693 SerGlyAlaHisValValLeuAspAspThrAspValGlyTrpValGluLysArgLys 712
Db      1708 WMSGNGCNCATGNTNTNTNGAYGAYGACAGATGNGNTAYGTNARGAYGNGNACN 1767
Oy      713 ProCysGlyProSerMetCysLeuAspArgLysCysLeuGlnIleGlnAlaLeuAsn 732
Db      1768 CCNTGYGNCNMSNATGATGTGYTNGAYMGNAARTGYTNCARATHCARGCNTNNAAY 1827
Oy      733 MetSerSerCysProLeuAspSerLysGlyLysValCysSerGlyHisGlyValCysSer 752
Db      1828 ATGWSMWSNTGYCCNTNCAIYWSNARAGNAARGATMTGWMSGNCAVGGNGTNGWSN 1887
Oy      753 AsnGluAlaThrCysIleCysAspPheThrTrpAlaGlyThrAspCysSerIleArgAsp 772
Db      1888 AAYGARGCNCNCTGYATHTGAYTAYACNTGGCGNCGNCAAYTGYWSNATHMGNGAY 1947
Oy      773 ProValArgAsnLeuHisProProLysAspGlnGlyProLysGly 787
Db      1948 CCNCTNMGNAAYTNCAYCCNCAARGATGARGNCCNAARGN 1992

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## RESULT 5

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US-09-809-617-3
: Sequence 3, Application US/09809617
: Patent No. US20020137178A1
: GENERAL INFORMATION:
: APPLICANT: Sheppard, Paul O.
: APPLICANT: Balindur, Nand
: APPLICANT: Delsher, Theresa A.
: APPLICANT: Bishop, Paul D.
: TITLE OF INVENTION: DISTINTEGRIN HOMOLOG
: FILE REFERENCE: 98-29
: CURRENT APPLICATION NUMBER: US/09/809,617
: PRIOR FILING DATE: 2001-03-15
: PRIOR APPLICATION NUMBER: US/09/351,414
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 3
: LENGTH: 2088
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: zdin1 amino acid degenerate sequence
: NAME/KEY: variation
: LOCATION: (1)...(2088)
: OTHER INFORMATION: n is any nucleotide
: NAME/KEY: misc_feature
: LOCATION: (1)...(2088)
: OTHER INFORMATION: n = A,T,C or G
: US-09-809-617-3

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Alignment Scores:
Pred. No.: 3, 84e-300
Score: 3007.00
Percent Similarity: 80.61%
Best Local Similarity: 80.61%
Query Match: 66.04%
DB: 10
Matches: 2088
Conservative: 528
Mismatch: 127
Indels: 0
Gaps: 0

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US-09-634-252A-4 (1-832) x US-09-809-617-3 (1-2088)

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Db	28	GAYACMAARCGNMGCATCARGARARAYAAAYARCGNGTNCATYTTMGCCARCCNM	87
QY	153	PheGlnIleGluAlaAaPheGlySerLysPheIleLeuAspLeuIleLeuAsnAsnGlyLeu	172
Db	88	TTYCARATHTGARGCNTTGGNMWNAARFTYATHYTCNGAYTTNATHTYTNAAAYAAAGNYTN	147
QY	173	LeuSerSerAspIyIyValGluIleHisIyTrGLuAsnGlyLysProGlnItySerLysGly	192
Db	148	YTNMSNMNSNGAYTYAGTNGARATCAATAYARAAYGGNAARCCCATPAAWNAARCGN	207
QY	193	GlyIleuHisCysTYrTYrHisGlySerIleArgGlyValLysAspSerLysValaIleLeu	212
Db	208	GGNARCAATYTYTATCAATGAGMWSNATHTHNGNGNGTNAARGAATWISNAARCTNCCNTTN	267
QY	213	SerThrCysAsnGlyLeuHisGlyMetPheGluAspAspThrPheValTYrMetIleGlu	232
Db	268	WSNACNTNGYAAAGNNTWCAYGAGNATGTYTGARCAATGAYACNTTGGYNTAAATGATHGARG	327
QY	233	ProLeuGluLeuValhIsAspGluLysSerThrGlyArgProHisIleIleGlnIySthr	252
Db	328	CCNTTNGARITYTNGTNCATGATGARARARMSNACNGMGCNCATAYATATTCARARACN	387
QY	253	LeuAlaGlyGlnTYrSerLysGlnMetLysAsnLeuThrMetGluAlaGlyAspGlnTrp	272
Db	388	YTNCCNGCNGCARTYAWWNAARCAATGARAAYATTNACNATGARGARMSNGNGATYCARITGG	447
QY	273	ProPheLeuSerGluLeuGlnTrpLeuLysArgGlyAsArgAlaValAsnProSerArg	292
Db	448	CCNTTYTNNMSGARITYTNCATGTGTTNARMGNMGNARMRMGNGNGYNAATCCNMNSMGN	507
QY	293	GlyIlePheGluGluMetLysTYrLeuGluLeuMetIleValAsnAspHisLysThrTYr	312
Db	508	GGNATHTTYTGARGARATGAARTAYTTNGARTTNATGATHGGAAAGATCAATAAARCNATY	567
QY	313	LysLysHisArgSerSerHisAlaHisThrAsnAspPheAlaLysSerValaAsnLeu	332
Db	568	AARARCAAYCMNSMNSMNCAYGCNCAYACNAAYATTYGCAARARMSNGTNGTNAAYTYN	627
QY	333	ValAspSerIleTYrLysGluGlnLeuAsnThrArgValaValLeuValaValaGluThr	352
Db	628	GTNCATYSNATHTTYAARGARCAATYTNAAAYCCNMGNGTNGTNYTNGTNGCCTNARACN	687
QY	353	TYrThrGluLysAspGlnIleAspIleThrThrAsnProValAGlnMetLeuHisGluPhe	372
Db	688	TGCACNGARARAGAYCARATHTGATATNCCNMCAATCCNGTNCARARCTYTNCAATYARTTY	747
QY	373	SerLysTYrArgGlnArgIleLysGlnHisAlaAspAlaValhIsLauIleSerArgVal	392
Db	748	WSNARARAYMCMNCARMGNATHAARCAARAYCCNGAYCCNGTNCAYTNAATHMSNMNGCTN	807
QY	393	ThrPheHisTYrLysArgSerSerLeuSerTYrPheGlyGlyValaCysSerArgThrArg	412
Db	808	ACNTTYCATYTYAARMGMSMWSNVTNMSNTATYTYTGARGGNGTPTYYSWMSNMGNAACNMGN	867
QY	413	GlyValaGlyValaAsnGluTYrGlyLeuProMetAlaValaIleGlnValLeuSerGlnSer	432
Db	868	GGCTGTGCGNGTNGNAAAYGARTAYGAGTNTCCNATGTGCGTNGTNCARCTYTWMSNCAARMSN	927
QY	433	LeuAlaGlnAsnLeuGlyIleGlnTrpProSerSerArgLysProLysCysAspCys	452
Db	928	YTNCCNCAARAYTYTNGNATHTCATRTGGARGCCNMMSNMGNAAARCCNAARFGTCAATGY	987
QY	453	ThrIleSerTrpGlyGlyCysIleMetGluGluThrGlyValaSerHisSerArgLysPhe	472
Db	988	ACNGARMSNTGGCGNGTGYATATGATGARBARACNGNGTMSNCATWISNMGNAAARTTY	104
QY	473	SerLysCysSerIleLeuGlnTYrArgAspPheLeuGlnArgGlyGlyValaCysLeu	492
Db	1048	WSNARATGYSWNAATHYTGARTAAWNGNAATYTYTNNARMGNGGNGMNGCTNGYTYTN	1107

493 PheAsnArgProThrLysLeuPheGluProThrGluCysGluAsnGlyIleValGluAla 512  
 1108 TTTAAATMGCCCAACNAAARTNTTTTGARCCNACNGARTGTGGNAAATGNTATGNGARGCN 116  
 513 GluGluGluCysAspCysGlyPheHisValGluCysTyrGlyLeuCysCysLysLysCys 532  
 1168 GGNARGARTGTGAVTGTGCGNTTTCATGNTNGARTGTATGCGNTTNGTGTGAARAAARTGT 122  
 533 SerLeuSerAsnGluAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCysLeu 552  
 1228 WSNYTNWMSAAAGCGMGCCNCAATGCGMSNGAATGCGNCCNTGTGTGAATGAAYCAACMSNTGTGTTN 128  
 553 PheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGlyTyr 572  
 1288 TTYCARRCCMMGNGNTATGARTGTGMNGAATGCGNTNAAAGARTGTATATACNGARTAT 134  
 573 CysThrGlyAspSerGlyGlnCysProProAsnLeuHisLysGlnAspGlyTyrAlaCys 592  
 1348 TGYACNGGGAATWSNNGNCARRGTGCGNCCNAAATYTNCAATAARARARATYGGNTATG 140  
 593 AsnGlnAsnGlnGlyArgCysTyrAsnGlyGluCysLysThrArgAspAsnGlnCysGln 612  
 1408 AAYCARAAACAGAGMNGNTGTATATGAAGCGNGARTGTAAARACMNGNCAATGAAYCARTGTGAR 146  
 613 TyrIleThrGlyThrLysAlaIleGlySerAspLysPheCysTyrGluLysLeuAsnThr 632  
 1468 TATATHTGGGACNAAARCCNCCNCGMSNGAATATTTTGTATATARARARTTAAATACN 152  
 633 GluGlyThrGlnLysGlyAsnCysGlyLysAspGlyAspArgTrrIleGlnCysSerLys 652  
 1528 GARGGNACGARARARAGNAAATGTGCGNAAARGAATGAGMNTGCATHTCARTGTWSNAAR 158  
 653 HisAspValPheCysGlyPheLeuLeuCysThrAsnLeuThrArgAlaProArgIleGly 672  
 1588 CAYGAGTNTTGTGTGCGNTTGTNTTGTACNAAATYTNACMNGNCCNCCMGMNATHGGN 164  
 673 GlnLeuGlnGluIleIleProThrSerPheTyrHisGlnGlyArgValIleAspCys 692  
 1648 CARRTNCARGAGARRTHATHTCCNMACMSNTTATATCAATCARAGNAGNNGNATHGATGT 170  
 693 SerGluAlaHisValValLeuAspAspAspThrAspValGlyTyrValGluAspGlyThr 712  
 1708 WSNNGNCCCAATGNTNTNGATGAATGACNCAATGNTGNGMNTATGTNGARGATGSGNAC 176  
 713 ProCysGlyProSerMetCysLeuAspArgLysCysLeuGlnIleGlnAlaLeuAsn 732  
 1768 CCNTGTGGCCMWSNATGATGTGTYTNGAATGATGTYTNCARRTHCARGCNTYTAAT 182  
 733 MetSerSerCysProLeuAspSerLysGlyLysValCysSerGlyHisGlyValCysSer 752  
 1828 AATGWSNMSNTGTCCNTNTNGATYSNNAARGNNAARGNTTGTWSNCGNCAATGAGNGTNTGWSN 188  
 753 AsnGluAlaThrCysAlaIleCysAspPheThrTrpAlaGlyThrAspCysSerIleArgAsp 772  
 1888 AATGARGCACACTGTGATHTGTGATYTTACNTGGCGNAGNCAATGTGWSNATHMNGAT 194  
 773 ProValArgAsnLeuHisProProLysAspGluGlyProLysGly 787  
 1948 CCNGTNGMAAATYTNCAATGCCNCAARGAATGARGGNCNCAARGCN 1992

RESULT 6  
 US-09-792-200B-17  
 ; Sequence 17, Application US/09792200B  
 ; Patent No. US20020042368A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Immunex Corporation  
 ; APPLICANT: Fanslow, William C.  
 ; APPLICANT: Poindexter, Kurt  
 ; APPLICANT: Cerretti, Douglas P.  
 ; APPLICANT: Black, Roy A.  
 ; TITLE OF INVENTION: INTEGRIN ANTAGONISTS  
 ; FILE REFERENCE: 2958-A

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: CURRENT APPLICATION NUMBER: US/09/792, 200B
: CURRENT FILING DATE: 2001-02-23
: PRIOR APPLICATION NUMBER: US 60/184, 865
: PRIOR FILING DATE: 2000-02-25
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 17
: LENGTH: 1668
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Fusion Construct
: NAME/KEY: CDS
: LOCATION: (25)..(1647)
: OTHER INFORMATION:
US-09-792-200B-17

Alignment Scores:
Pred. No.: 2,4e-163 Length: 1668
Score: 1680.00 Matches: 288
Percent Similarity: 99.31% Conservative: 0
Best Local Similarity: 99.31% Mismatches: 2
Query Match: 36.90% Indels: 0
DB: 10 Gaps: 0

US-09-634-252a-4 (1-832) x US-09-792-200B-17 (1-1668)
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Db 85 ACTAGTGTGGAATGATGATACGTCGAGAGCTGGGAGAGAGTGTGATGTTGCATTCAGTGTG 144
QY 523 GlucylTyrGlyLeuGlyCysGlyLysCysSerLeuSerAsnGlyAlaHisCysSerAsp 542
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Db 145 GAATGCTATGATGATATCTGTAGAGAAATGTTCCCTCTCCAAAGGGGCTCACTGCGAGGAC 204
QY 543 GlyProCysAsnAsnThrSerCysLeuPheGlnProArgGlyTyrGlyCysArgAsp 562
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Db 205 GGGCCCTGCTGTAACATACCTCATGCTTTTTCAGCCAGCAGGCTATGAATGCCGGGAT 264
QY 563 AlaValAsnGlyCysAspIleThrGlyTyrCysThrGlyAspSerGlyLysCysProPro 582
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 265 GCTGTGAACGAGTGTGATATGATGATATGCTGAGACTGTGGTCACTGCGCCACCA 324
QY 583 AsnLeuHisLysGlnAspGlyTyrAlaCysAsnGlnAsnGlnGlyArgCysTyrAsnGly 602
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 325 AATCTTCTAAGACAGAGGATATGCAATCAATAAATCCAGGGCCGCTGTACATGCG 384
QY 603 GlucylsThrArgAspAsnGlnCysGlnTyrIleTyrGlyThrLysAlaAlaGlySer 622
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Db 385 GAGTGCAGAGCCAGACAGACACAGTGTCAATCTGGGGAACAAGGCTGACAGGCTCT 444
QY 623 AspLysPheCysTyrGlyLysLeuAsnThrGluGlyThrGlyLysGlyAsnGlyLys 642
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 445 GACAAGTCTGCTATGAAAGAGCTGAATACAGAAAGCACTGAGAAAGAACTGCGGAG 504
QY 643 AspGlyAspArgTyrIleGlnCysSerLysHisAspValPheCysGlyPheLeuLeuLys 662
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 505 GATGAGACCGGTGATTCAGTCAAGCAACATGATGTTGTTCTGTGATCTTACTCTGT 564
QY 663 ThrAsnLeuThrArgAlaProArgIleGlyGlnLeuGlnGlyLysIleIleProThrSer 682
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 565 ACCAATCTTACTCGAGCTCCAGCTTGTGTCACCTTCACGGGTGATATCATTCACACTTCC 624
QY 683 PheTyrHisGlnGlyArgValIleAspCysSerGlyAlaHisValValLeuAspAsp 702
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 623 TTTCTACATCAAGCGCGGTGATGATGCTGACAGTGTGCTGATGTTTATGATGATGAT 684
QY 703 ThrAspValGlyTyrValGluAspGlyThrProCysGlyProSerMetMetCysLeuAsp 722
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Db 685 ACGGATGTGGCTATGATAGATGAGAACGCAATGTGGCCCTGTATGATGTGTGTTAGAT 744
QY 723 ArgGlyCysLeuGlnIleGlnAlaLeuAsnMetSerSerCysProLeuAspSerLysGly 742
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Db 745 CGAAGTGCCTACAAATTCACCCCTAAATATGACGAGCTGTCCAGTCCAGGCT 804
QY 743 LysValCysSerGlyHisGlyValCysSerAsnGlnAlaThrCysIleCysAspPheThr 762
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 805 AAGTGTGTGGGCGCCATGGGTGTGTACTAATGAAGCACCAGCTGATTTGTATTCACC 864
QY 763 TrpAlaGlyThrAspCysSerIleArgAspProValArgAsnLeuHisProProLysAsp 782
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 865 TGGCGAGGACAGATTCAGTATCCGGGATCCAGTTAGAACCTTCACCCCCCAAGAT 924
QY 783 GluGlyProLysGlyProSerAlaThrAsn 792
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 925 GAAGACCCCAAGGCTCTAGTGCACCAAT 954

RESULT 7
US-10-020-733-9
: Sequence 9, Application US/10020733
: Patent No. US20020161214A1
: GENERAL INFORMATION:
: APPLICANT: Walke, D. Wade
: APPLICANT: Wilgenowski, Nathaniel L.
: APPLICANT: Fiddie, Carl Johan
: TITLE OF INVENTION: NO. US20020161214A1el Human Proteases and Polynucleotides Enco
: FILE REFERENCE: LEX-0263-USA
: CURRENT APPLICATION NUMBER: US/10/020,733
: PRIOR APPLICATION NUMBER: US/10-10-30
: PRIOR FILING DATE: 2000-11-01
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 9
: LENGTH: 3512
: TYPE: DNA
: ORGANISM: homo sapiens
US-10-020-733-9

Alignment Scores:
Pred. No.: 1,05e-95 Length: 3512
Score: 1029.50 Matches: 266
Percent Similarity: 44.35% Conservative: 115
Best Local Similarity: 30.97% Mismatches: 341
Query Match: 22.61% Indels: 137
DB: 9 Gaps: 31

US-09-634-252a-4 (1-832) x US-10-020-733-9 (1-3512)
QY 4 ProGlySerSerSerArgGlnProProLeuAlaGlyCysSerLeuAlaGlyAlaSerCys 23
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 52 CTTCTTCATATCTCGGAGAGCCCGGAGGCTGAGCGGAGCGTTCGACAGAGGCTGAGCGG 111
QY 24 GlyProGlnArgGlyProAlaGlySerValProAlaSerAlaPro----- 38
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 112 GTGGGAGAGCGCGGGGCGAGCGGGGGTTCAGACGGCGGCTCCACGCGCGGCGAGTGG 171
QY 39 -----AlaArgThrProPro--- 43
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 172 CAGTATGCTGAGGCGCTGTGAGCGCGGAGCGGCTAAGGGCGCGGCCACCATGCGAGG 231
QY 4 -----CysArgLeuLeuLeuValLeuLeuLeuLeuLeuProProLeuAlaAlaSer 59
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 232 GCGCGAGGCGCGCGCGCTGCTGTGGCGCTTGGCTGTGACAGCCCTC----- 282.
QY 60 SerArgProArgAlaTrpGlyValAlaAlaProSerAlaProHisIleTrpAsnGlyThrAla 79
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 283 ---CGGCGCGG-----CGCGCGCGGAGCGCTGATGGACAAGAGAGAGT 324
QY 80 GluLysAsnLeuGlyValLeuAlaAspGluAspAsnThrLeuGlnGlnAsnSerSerSer 99
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 325 GAGGAAGC----- 333
QY 100 AsnIleSerTyrSerAsnAlaMetGlnGlyIleThrLeuProSerArgLeuIleTyr 119
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 334 -----AGCCCAAGCTGCGACATGTAATTCATACCTCAGTGG----- 372
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QY 120 TyrTLeaenGlnAspSerGluSerProTyrHisValLeuAspThrLysAlaArgHisGln 139  
 Db 373 -----AAGACTTCAGAAAGCCCGTG----- 393  
 QY 140 GlnLysHisAsnLysAlaValHisLeuAlaGlnAlaSerPheGlnIleGlyAlaPheGly 159  
 Db 394 -----AGAGAAAGACTCCCTCAAACTGAGCTGAGCTAATGCGTGGAGGG 441  
 QY 160 SerLysPheIleLeuAspLeuIleLeuAsnAsnGlyLeuLeuSerSerAspTyrValGlu 179  
 Db 442 CGAAGACTGATCTGGAGCTGGAGAGAGATGAGCAACTTTTGGCTTCCTTCCAGAGAA 501  
 QY 180 IleHisTyr---GluAsnGlyLysProGlnTyrSer-----LysGlyGlyGlnHisCys 196  
 Db 502 ACCCATATATCTCACTGATGGAACCTGAAACCAACAGCGAATGGAAGATCACTGC 561  
 QY 197 TyrTyrHisGlySerIleArgGlyValLysAspSerLysValAlaLeuSerThrCysAsn 216  
 Db 562 TTTTACACGCGAGCGTGGAGAGACAGACTGTCAGCGCTCAGCACTTGGCGGA 621  
 QY 217 GlyLeuHisGlyMetPheGlu---AspAspThrPheValTyrMetIleGluProLeuGlu 235  
 Db 622 GGAATTTAGAGACTGATTTAGCGTGAGAGACCACTCAGCTGATCGAGCCCTCCCT 681  
 QY 236 LeuValHisAspGlyLysSerThrGlyArgProHisIleIleGlnLysThrLeuAlaGly 255  
 Db 682 -----GACACCAAGGGC-----CAACACCTTATTTACAA----- 711  
 QY 256 GlnTyrSerLysGlnMetLys-----AsnLeuThrMetGluArgGlyAsp-- 270  
 Db 712 -----TCGTGACATCTCAAGCCCGCCCGGAAACTGTGGGTTCGCACTCCAAACCC 765  
 QY 271 -----GlnTyrProPheLeuSerGluLeuGlnIlePheLysAlaArgLysArgAla 287  
 Db 766 ACCACCGAGGAGCTGGGCT---CTTCAGTTTACACAGACAGCAAGAGCGCGCTCGAGG 822  
 QY 288 ValAsnProSerArgGlyIlePheGluGluMetLysTyrLeuGluLeuMetIleValAsn 307  
 Db 823 ATG-----AAAGGGAAGATTTAACTCCATGAGATGCGAGCTTACCTGCTGGCT 876  
 QY 308 AspHisLysThrTyrLysLysHisArgSerSerHisAlaHisThrAsnAsnPheAlaLys 327  
 Db 877 GATTATTAGAGCTTTCAGAGAAATGAGAGACAGACAGACCGCCACCAACAACTCAT 936  
 QY 328 SerValValAsnLeuValAspSerIleTyrLysGluGlnLeuAsnThrArgValLeu 347  
 Db 937 GAGATCGCCACACTGATGATTAAGTTTACCGA---TCCTTGAACATCCGGATTGCTCTC 993  
 QY 348 ValAlaValAlaGluThrTyrThrGluLysAspGlnIleAspIleThrLysAsnProValGln 367  
 Db 994 GTGGGCTTGAAGTGTGAGCCACGAGACATGTGTGAGATTCAGAGAAATCCATATTCT 1053  
 QY 368 MetLeuHisGluPheSerLysTyrArgGlnArgIle-----LysGlnHisAlaAspAla 385  
 Db 1054 ACCCTGTGGCTCTTCTCAGTTGGAGCGCAAGCTGCTCCCGCAGAGTACCAATGCAAC 1113  
 QY 386 ValHisLeuIleSerArgValThrPheHisTyrLysArgSerSerLeuSerTyrPheGly 405  
 Db 1114 GCCCAATTAATCACGGGAGCTCTTCCACGGACACCACTCGGCTCGGCCCTCATG 1173  
 QY 406 GlyValCysSer-----ArgThrArgGlyValGlyValAsnGluTyrGlyLeuProMet 423  
 Db 1174 GCCATGTGCTCTGTGACAGTGTGAGAGACTGAACATGAGCCACTCGAGAAATGCCATT 1233  
 QY 424 AlaValAlaGlnValIleuSerGlnSerLeuAlaGlnAsnLeuGlyIleGlnTyrGluPro 443  
 Db 1234 GCGCTGTGCTGCGACCATGCGCCAGAGATGGCCCAACTTGGCAAGACCATGATCTCT 1293  
 QY 444 SerSerArgLysProLysCysAspCysThrGluSerThrGlyGlyCysIleMet---Glu 462  
 Db 1294 GCAAT-----TCGTGCTCGGCGAGTGGGCTGATGTGGGTGATCATGAGCACT 1344

QY 463 GlnThrGlyValSerHisSerArgLysPheSerLysCysSerIleLeuGluTyrArgAsp 482  
 Db 1345 GCCACTGGGACACCCCTTCCCAAGTGTTCATGATGAGCAAGAGAGAGCTGGACAG 1404  
 QY 483 PheLeuGlnArgGlyGlyGlyValAlaCysLeuPheAsnArgPro-----ThrLysLeuPhe 500  
 Db 1405 TATCTGACAGTGTGCTGTGATGTCTCTCCAACTGACAGACACAGCATGTTGAT 1464  
 QY 501 GluProThrGluCysGlyAsnGlyTyrValGlnAlaGlyGluGlyCysAspCysGlyPhe 520  
 Db 1465 GGAGCGCGAGCTGTGGAGAGGGATATCTGGAAGATGGAAGAGTGTGACTGTGGAGA 1524  
 QY 521 HisValGluCysTyrGlyLeuCysCys-----LysLysCysSerLeuSerAsnGlyAla 538  
 Db 1525 GAACAGAAATGTATCAACACCCCTGCTGCAATGCTCTAATTTATACCTGAGGCGGGGCG 1584  
 QY 539 HisCysSerAspGlyProCysCysAsnAsnThrSerCysLeuPheGlnProArgGlyTyr 558  
 Db 1585 GAGTGTCTCTACGCGCTCTGCTGCCAC-----CAGTGTAAAGCTGTGGCTCTGGGACC 1638  
 QY 559 GluCysArgAspAlaValAlaGlnCysAspIleThrGluTyrCysThrGlyAspSerGly 578  
 Db 1639 CTGTGCGCGAGAGCGGACGAGCATGTGACCTCCCGAGATTCTGTACGGGCACTCTCC 1698  
 QY 579 GlnCysProProAsnLeuHisLysGlnAspGlyTyrAlaCysAsnGlnAsnGlnGlyArg 598  
 Db 1699 CACTGCGCTTACCACTTCTACCAAGATGATGATGATGATGATGATGATGATGATGAT 1758  
 QY 599 CysTyrAsnGlyGlyCysLysThrArgAspAsnGlnCysGlnTyrIleThrGlyThrLys 618  
 Db 1759 TGTCTACAGCGCATGTGCTCTACCTACAGAGAGAGTGCAGCGAGCTGTGGGACCGCGA 1818  
 QY 619 AlaAlaGlySerAspLysPheCysTyrGlyLysLeuAsnThrGluGlyGluGly 638  
 Db 1819 GCCCGACCTGCGCTGACCTGCTGCTGAGAGGTGATGATGATGATGATGATGATGATGAT 1878  
 QY 639 AsnCysGlyLysAsp---GlyAspArgTyrIleGlnCysSerLysHisAspValPheCys 657  
 Db 1879 AACTGTGGAAGAGCATGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1938  
 QY 658 GlyPheLeuLeuCysThrAsnLeuThrArgAlaProArgIleGlyGlnLeuGlnGlyGlu 677  
 Db 1939 GGGAGATGCTCAGTGTGAGCTGAGCTGAGCGCGCGCC-----CTGGAGCTCCAAAC 1986  
 QY 678 IleIlePro-----ThrSerPheTyrHisGlnIleArgValIleAspCysSerGlyAla 695  
 Db 1987 GCGGTGCCCATTTGACACCACTATCATGATGATGATGATGATGATGATGATGATGATGAT 2046  
 QY 696 HisValValLeu-----AspAspAspThrAspValGlyTyrValGluAsp 710  
 Db 2047 CACTGTACAGAGCTCTGAGAGAGAGGATGATGATGATGATGATGATGATGATGATGATGAT 2106  
 QY 711 GlyThrProCysGlyProSerMetMetCysLeuAspArgLysCysLeuGlnIleGlnAla 730  
 Db 2107 GGAACCAAGTGTGCTCAACCAATATTGCTTGAAGGGCGAGTGCAGAGAACACTCTTC 2166  
 QY 731 LeuAsnMetSerSerCysProLeuAspSerLysGlyLysValLysSerGlnHisGlyVal 750  
 Db 2167 TTTTAAACTGAAGCTGT-----GGAGAAAGATGATGATGATGATGATGATGATGATGAT 2211  
 QY 751 CysSerAsnGlnAlaThrCysIleCysAspPheThrTrpAlaGlyThrAspCysSerIle 770  
 Db 2212 TGTAAACAACAACAGAACTGCTGCTGCGGGCGGGCGCGCGCTTGTGACACCA 2271  
 QY 771 ArgAspProValAlaGlnLeuHisProProLysAspGluGlyProLysGlyProSerAla 790  
 Db 2272 CCGGCGCAAGGGGCGACTATC-----GACAGTGGCGCTTATGCCCGCGAGAGT 2319  
 QY 791 ThrAsnLeuIleIleGlySerIleAlaGlyAlaIleLeuValAlaIleValLeu 809  
 Db 2320 GTGGGCTGTGTGATGCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 2376

RESULT 8









Db	97	GGAGTGTGAGAAAGGC-----	111
Oy	98	SerSeranIleSerTyrSerAsnAlaMetGlnIysGluIleThrLeuProSerArgLeu	117
Db	112	-----AGCCCCAAGCTGCGACATGAACCTTATCATACCTCAGTGG---	150
Oy	118	IleTyrTyrIleAsnGlnAspSerLeuSerProTyrHisValLeuAspThrIysAlaArg	137
Db	151	-----AAGACTTCAGAAACCCCCGTC-----	171
Oy	138	HisGlnGlnIysHisAsnLysAlaValHisLeuAlaGlnAlaSerPheGlnIleGluAla	157
Db	172	-----AGAGAAAGCATCCACATCAAGCTGAGAGCTCAGGGTAATGGCT	213
Oy	158	PheGlySerLysPheIleLeuAspLeuIleLeuAsnAsnGlyLeuLeuSerSerAspTyr	177
Db	214	GAGGGGCGAGAACTGATCTCGACTCGGAGAGAAATGACCAACTTTTTCCTCTCTCTAC	273
Oy	178	ValGluIleHisTyr-----GluAsnGlnLysProGlnIleTyrSer-----LysGluGlyGlu	194
Db	274	ACAGAAACCCATTATACCTTCAAGTGTGAACCTCAACACACACACAGAAATTTGGAGAT	333
Oy	195	HisCysTyrTyrHisGlySerTyrLeaArgLysAlaLysAspSerLysValAlaLeuSerThr	214
Db	334	CAGCTCTTTTACACGGCACGGTGGAGACAGAACTGTCCAGCGTCAAGCTCAGCTCAGCACT	393
Oy	215	CysAsnGlyLeuHisGlyMetPheGlu---AspAspThrPheValTyrMetIleGluPro	233
Db	394	TGCCGAGGAATTAGAGACGTGATTACGGTGACACACACACCTCAGCTACGTCAATCGAGGCC	453
Oy	234	LeuGlnLeuValHisAspGlnLysSerThrGlyArgProHisIleIleGlnIlySerThrLeu	253
Db	454	CTCCCT-----GACACGAAAGCGC-----CAACACCTTATTATACAGA-----	489
Oy	254	AlaGlyGlnTyrSerLysGlnMetLys-----AsnLeuThrMetGlnArgGly	269
Db	490	-----TCTGAACATCTCAAGCGCGCCCGGGAAGACTGTGGCTTGACGACCTCC	537
Oy	270	Asp-----GlnTyrProPheLeuSerGlnLeuGlnIleTyrLeuAspArgLys	285
Db	538	AAGCCACACACAGAGCTGGGCT---CTTCAGTTTACCAACAGACCAAGAAAGCAAGCT	594
Oy	286	ArgAlaValAsnProSerArgGlyIlePheGlnGlnMetLysTyrLeuGlnLeuMetIle	305
Db	595	CGCAGGAGTG-----AAAAGGAAAGATTAAATCCTCATGAAATATGTGGAGCTTTAACTTC	648
Oy	306	ValAsnAspHisLysThrTyrLysLysHisArgSerSerHisAlaHisHisAsnPhe	325
Db	649	GTGGCTGATTTATTAGACTTTCAGAGAAGATCGACAGACACAGACGCCCAACACCAAG	708
Oy	326	AlaLysSerValValAsnLeuValAspSerIleTyrLysGlnGlnLeuAsnThrArgVal	345
Db	709	CTCATAGACATCGCCCACTATGTTATGAATTTTACCGCA---TCCATTGAACATCCGGATT	765
Oy	346	ValLeuValAlaValGlnThrTyrPheGlnLysAspGlnIleAspIleThrIlyAsnPro	365
Db	766	GCTCTCGTGGCTTGGAAAGTGTGACCCACAGCGGAACATGTGGAAGTTTCAAGAAATTC	825
Oy	366	ValGlnMetLeuHisGlnPheSerLysTyrArgGlnArgIle-----LysGlnHisAla	383
Db	826	TATTCTACCTCTGTGCTTCTCTCAGTTGGAGCGCCAAAGCTCTTGCCCAAGATTCAT	885
Oy	384	AspAlaValHisLeuIleSerArgValIlePheHisTyrLysArgSerSerLeuSerTyr	403
Db	886	GACAAAGCCCAATTATATACGGGCAATGTCCTTCCACGGCACACCAACACGCGTGGCCCCC	945
Oy	404	PheGlyGlyValLysSer-----ArgThrArgGlyValGlyValAsnGlnIlyArgIleu	421
Db	946	CTCATGGCCATCTGCTGTCTGTACCAAGTCTGGAGAGATCAATGACATCCACCTCCAGAAT	1001
Oy	422	ProMetAlaValAlaGlnValLeuSerGlnSerLeuAlaGlnAsnLeuGlyIleGlnTyr	441

Db	1006	GCATATTGGCGTGGCGCCACCATTGGCCACGAGATGGCCACAACTTTGGCATGGCCAT	10655
OY	442	GLUPROSERSerArGlyLysProLysCysAspCysThrInGluSerThrPGLyGLyCysIleMet	461
Db	1066	GATTCCTCGAGAT-----TGCCTGCGCCCACTGGCGCGATGGGGTGCATCATG	1116
OY	462	--GluGluThrInGlyValSerHisSerArgLysPheSerLysCysSerIleLeuGluYr	480
Db	1117	GCAGTGGCACTGGGCAACCCCTTTCCCAAGTGTTCATGTGATGCACAGAGGAGGACTG	1176
OY	481	ArgAspPheLeuGlnArgGLyGLyGLyValaCysLeuPheAsnArgPro-----ThrLys	498
Db	1177	GACAGGTATGTGCAAGTCAAGTGGTGGATGTGTCTCTCCACATGCTCCAGACACGAGATG	1238
OY	499	LeuPheGluProThrInGlyCysGLyAsnGlyYrValIGluAlaGLyGluGlyCysAspCys	518
Db	1237	TTTGATGGAGGCCCGGAGGTGTGGGAACGGATATCTGGAAGAATGGGGAAGATGTGACGT	1296
OY	519	GLYPheHisValaGLyCysTyrgLyLeuGlyCys-----LysLysCysSerLeuSerAsn	536
Db	1297	GGAGAAGAAGAGMATGTACACACCCCTGCTGCATGGCTTAATTTGATACCTTGAGGCCG	1356
OY	537	GLyAlaHisCysSerAspGLyProCysCysAsnThrSerCysLeuPheGlnProArg	556
Db	1357	GGGGGGGAGTGTGCTCACGGCTCTGCGTCCGAC-----CAGGTAAACCTTGTGGCTCT	1410
OY	557	GLYTrGLyCysArgAspAlaValaAsnLysCysAspIleThrInGlyTrCysThrInGlyAsp	576
Db	1411	GGGACCCCTGTGCCCGGACGACGACGACGAGTGTACCTCCGGAAATTTGTAGGGGCAAG	1470
OY	577	SerGLyGlyCysProProAsnLeuHisLysGlnAspGLYTrAlaCysAsnGlnAsnGln	596
Db	1471	TCTCCCCCACTGCTACCAACATTTCTACAGATGTGATGGTACCCTCTGAGAGGGGGCCAG	1530
OY	597	GLyArgCysTyrrAsnGLyGLyCysLysThrArgAspAsnGlyGlnTyrIleIrrpGLy	616
Db	1531	GCCTAAGTCTACACAGCGCATGTGCTTCACCTPACAGAGCAGATGCCACACTGTGGGGA	1590
OY	617	ThrLysAlaIaGLySerAspLysPheCysTyrgLysLeuAsnThrGLyGLyTrGlu	636
Db	1591	CCCGGAGCCGACCGCCCTGACCTCTGCTTCGAGAAAGTGATGTGGCAGAGACACAC	1650
OY	637	LysGLyAsnCysGLyLysAsp---GLyAspArgTrIleGlyCysSerLysHisAspVal	655
Db	1651	TTTGGAAACTGTGGAAAGACATGATTCGTACACACAGAAAGTGGTCACATGACAGATTCG	1710
OY	656	PheCysGLyPheLeuLeuCysThrAsnLeuThrArgAlaProArgIleGLyGluLeuGln	675
Db	1711	AAGTGTGGGAAGATTCAGTGTCAAGCTCTAGAGCCGCGCC-----CTGGAG	1758
OY	676	GLyGluIleIlePro-----ThSerPheTyrHisGlnGlyArgValIleAspCysSer	693
Db	1759	TCCAAAGCGGGGCTCATGACACACACATTCATGTAGATGGAGGACATGCAGTGGCCG	1818
OY	694	GLyAlaHisValaValLeu-----AspAspAspThrAspValIGlyYrVal	708
Db	1819	GGCAACCCACGTCATCCAGGATCTCTGAGAGGAGGAGGCTGCATCTGACACGACCGCTGGTG	1878
OY	709	GluAspGLYThrProCysGLyProSerMetLeuCysLeuAspArgLysCysLeuGlnIle	728
Db	1879	ATGACATGGAAACAGTGTGCTTACACACCATTTTGTCTTGAAGGGGCAATGCAGAACACC	1938
OY	729	GlnAlaLeuAsnMetSerSerCysProLeuAspSerLysGLyLysValaCysSerGLyHis	748
Db	1939	TCCATTCTTTGAAACTGAGAGCTGT-----GGGAAGAAATGTCAMATGCGCAT	1983
OY	749	GLyAlaCysSerAsnGluAlaThrCysIleCysAspPheThrTrpAlaGLYThrAspCys	768
Db	1984	GGGGTCTGTACAAACACACAACTGCCACATGCTCCGCGGGCTGGGCCCTTCTGTGC	2043
OY	769	SerIleArgAspProValaArgAsnLeuHisProProLysAspGLyGlyProLysGLYPro	788
Db	2044	AACACACCGGGCCACGCGGGGAGTATC-----GACAGTGGGCGCTATGCGCCCT	2093



[illegible]

	PRIOR APPLICATION NUMBER:	09/955,504	
	PRIOR FILING DATE:	2001-09-19	
	PRIOR APPLICATION NUMBER:	09/712,907	
	PRIOR FILING DATE:	2000-11-16	
	PRIOR APPLICATION NUMBER:	PCT/US00/14308	
	PRIOR FILING DATE:	2000-05-25	
	PRIOR APPLICATION NUMBER:	60/178,717	
	PRIOR FILING DATE:	2000-01-28	
	PRIOR APPLICATION NUMBER:	60/142,930	
	PRIOR FILING DATE:	1999-07-09	
	PRIOR APPLICATION NUMBER:	60/136,388	
	PRIOR FILING DATE:	1999-05-27	
	NUMBER OF SEQ ID NOS:	38	
	SOFTWARE:	Patentin Ver. 2.0	
	SEQ ID NO 2		
:	LENGTH:	2757	
:	TYPE:	DNA	
:	ORGANISM:	Homo sapiens	
:	US-10-125-452-2		
 Alignment Scores:			
Pred. No.:	1,34e-93	Length:	2757
Score:	1007.50	Matches:	252
Percent Similarity:	45.32%	Conservative:	111
Best Local Similarity:	31.46%	Mismatches:	325
Query Match:	22.13%	Indels:	113
DB:	9	Gaps:	29
 US-09-634-252A-4 (1-832) x US-10-125-452-2 (1-2757)			
OY	38	ProAlarGrThrProrocysArgLeuLeuValLeuLeuLeuProPtoleuAla	57
Db	4	CCAGGGGCGGCACGCCGCCGCCGCTTCGTGGCGTTTGCCTTGCAACCCCTC---	60
OY	58	AlaserSerArproarglAtprgIalAalAProserAlaproHistrpasGlu	77
Db	61	CGGCCGCGG-----CGCGCGCGGAGACTGATGACAAGA	96
OY	78	ThrAlaGlInLysAsnLeuGlyValLeuAlaaspGluasPasnThrLeuGlnGlnAsnSer	97
Db	97	GGAAGTAGAGAAAGGC-----	111
OY	98	SetSerAsnLieserTyrsertAsnLametGlnLysGluIleThrLeuProserArgLeu	117
Db	112	AGCCCCAAGCTGCAGCATTAATCATCTCACTGCG---	150
OY	118	IleTyrrTrIleasnGlnAspserGluSerProTyrrHisValLeuAspThrLysAlaArg	137
Db	151	AAGACTTCAGAAAGCCCCTG-----	171
OY	138	HisGlnGlnLysHisAsnLysAlaValHisLeuAlaGlnAlaSerPheGlnIleGluAla	157
Db	172	AGAGAAAAGCATCTCACTCAAAAGCTGAGAGCTGAGGCTAATGGCT	213
OY	158	PheGlySerLysPheIleLeuAspLeuIleLeuAsnAsnGlyLeuLeuSerSerAspTyrr	177
Db	214	GAGGGCGGAAGATGATCTCTGCACTGAGAGAAGATGACAACATTTCCTCTCTCTAC	273
OY	178	ValGlnIleHisTyrr--GluasnGlyLysProGlnTyrrSer-----LysGlyGlyGlu	194
Db	274	ACGAAACCATTATATCTCAAGTGTAACTCTCAAACACCAACAGGAAATTTGAGAGAT	333
OY	195	HisCysTyrrTyrrHisGlySerIleArgGlyValLysAspSerLysValAlaLeuSerThr	214
Db	334	CACCTGCTTTACACGCGCACGGGAGAGGACAGAACTGTCCAGGCTCACGCTCAGGACT	399
OY	215	CysAsnGlyLeuHisGlyMetPheGlu---AspAspThrPheValItyrMetIleGluPro	233
Db	394	TGCCGAGAGATTAGAGAGACTGATTACCGTGACACAGCAACCTCAGCTACGTATGAGACCC	453
OY	234	LeuGluLeuValHisAspLysLysSerThrGlyArgProGlnIleIleGlnLysThrLeu	253
Db	454	CTCTCT-----GACAGCAAGGCC-----CAACACTTATTATACAG-----	489

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Oy 254 AlaGlyGlnTyrSerLysGlnMetLys-----AsnLeuThrMetGluArgGly 269
Db 490 -----TCTGACATCTCAAGCCCGCCCGGAACCTGGGTTGACAGCACTCC 537
Oy 270 Asp-----GlnThrProPheLeuSerGluLeuGlnThrLeuArgArgLys 285
Db 538 AACCCACACACAGGAGCTGGGCT---CTTCACATTACACACAGCAACAGAACCCACT 594
Oy 286 ArgAlaValAsnProSerArgGlyIlePheGluGluMetLysTyrLeuGluMetIle 305
Db 595 CCGAGAGATG-----AAAGGGAAGATTTAACTCCATGACATGATGTGGAGCTTACCTC 648
Oy 306 ValAsnAspHisLysThrTyrLysLysHisArgSerSerHisAlaHisSerHisAsnPro 325
Db 649 GTGCTGATATTATTAGAGTTTCAGAAAGATCGACAGACAGACCCACCAACACACAG 708
Oy 326 AlaLysSerValAlaAsnLeuValAspSerIleTyrLysGluGlnLeuAsnThrArgVal 345
Db 709 CTCATAGAGATCGCCACATGTTGATAGTTTACCAG---TCCTTGAACATCCGGATT 765
Oy 346 ValLeuValAlaValGluThrTyrThrGluLysAspGlnIleAspIleThrAsnPro 365
Db 766 GCCTGCTGGGCTTGGCAAGTGTGACCCAGCCAGCAACATGTGTGAAGTTTCAGAGAAATCCA 825
Oy 366 ValGlnMetLeuHisGluPheSerLysTyrArgGlnArgIle-----LysGlnHisAla 383
Db 826 TATTCTACCCCTGCTGCTCTTCTCAGTTGGAGCGGCAAGCTGTGCCCAAGATACCAT 885
Oy 384 AspAlaValHisLeuIleSerArgValThrPheHisTyrLysArgSerSerLeuSerTyr 403
Db 886 GACACACCCCAATTAAATACAGGCGATGCTCTCCACGCGCACACCATCGGCGTGGCCCC 945
Oy 404 PheGlyGlyValLysSer-----ArgThrArgGlyValGlyValAsnGluTyrGlyLeu 421
Db 946 CTCATGGCAGATGCTGCTGTGTACACGCTGACAGTCAGATGACATGACACCACTCCAGAAAT 1005
Oy 422 PrometAlaValAlaGlnValLeuSerGlnSerLeuAlaGlnAsnLeuGlyIleGlnThr 441
Db 1006 GCCATTGGCGTGGCTGCCACCATGCGCCACAGATGCGCCACACTTGGGATACCAT 1065
Oy 442 GluProSerSerArgLysProLysCysAspCysThrGlnSerTyrGlyLysIleMet 461
Db 1066 GATTCTGCAAGT-----TGCTGCTGGGCGCACTGGCGGTGATGCGGTGCATCATG 1116
Oy 462 ---GluThrGlyValSerHisSerArgLysPheSerLysCysSerIleLeuGluTyr 480
Db 1117 GCAGCTGCCACTGGGACCCCTTCCCAAGTGTTCATGATGCAACAGACAGCGAGCTG 1176
Oy 481 ArgAspPheLeuGlnArgGlyGlyLysLysLeuPheAsnArgPro-----ThrLys 498
Db 1177 GACAGGTCTGCACTGAGTGTGTGAAATGTGTCTCCACATGCTCCAGACACCGAGATG 1236
Oy 499 LeuPheGluProThrGluCysGlyAsnGlyTyrValGluAlaGlyGluGlnCysAspCys 518
Db 1237 TTGTATGGAGCGCGGAGGTGTGGGAACGGATATCTGGAAGATGGGAAGAGTGTACTGT 1296
Oy 519 GlyPheHisValGluCysTyrGlyLeuCysCys-----LysLysCysSerLeuSerAsn 536
Db 1297 GGAGAAGAAGAGGATGTAACAACTGCTGCAATGCCCTTAATTGTAACCTTGAGGCGG 1356
Oy 537 GlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCysLeuPheGlnProArg 556
Db 1357 GGGGCGGAGTGTGCTACGCGCTCTGCTGCCAC-----CAGTGTAACTGTGGCTCCT 1410
Oy 557 GlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGluTyrCysThrGlyAsp 576
Db 1411 GGGACCCCTTGGCGGAGCAGGCGCAGGCGATGTGACCTCCGAGTTCGTGACGGGCAAG 1470
Oy 577 SerGlyGlnCysProPheAsnLeuHisLysGlnAspGlyTyrAlaCysAsnGlnAsnGln 596
Db 1471 TCTCCCACTGGCGCTTACCAACTTCTACAGATGATGATACCCCTGTGAGGCGGCGCAG 1530

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Oy 597 GlyArgCysTyrAsnGlyGluCysLysThrArgAspAsnGlnCysGlnTyrIleProGly 616
Db 1531 GCGTACTGCTACACAGCGCATGTGCTTCACTACAGAGCAGATGCGCACAGCTGTGGGA 1590
Oy 617 ThrLysAlaAlaGlySerAspLysPheCysTyrGlyLysLeuAsnThrGluGluThrGlu 636
Db 1591 CCCGAGCCCGAGCTGCGCTGACCTCTGCTTGGAGAGTGAATGTGTGCGCAGGACACACC 1650
Oy 637 LysGlyAsnCysGlyLysAsp---GlyAspArgTyrIleGlnCysSerLysHisAspVal 655
Db 1651 TTTGGAACTGTGGAAAGACATGAATGCTGAACACAGGAACATGCAACATGAGAGTGGG 1710
Oy 656 PheCysGlyPheLeuLeuMetCysThrAsnLeuThrArgAlaProArgIleGlyGlnLeuGln 675
Db 1711 AAGTGTGGGAAGATCCAGTGTGACAGCTCTGAGCCCGCGCC-----CTGGAG 1758
Oy 676 GlyGluIleLeuPro-----ThrSerPheTyrHisGlnGlyArgValIleAspCysSer 693
Db 1759 TCCAAACGCGGTGCCATTGACACCACTATTCATGATGAGAGGACAGATCCAGTCCGG 1818
Oy 694 GlyAlaHisValValLeu-----AspAspAspThrAspValGlyTyrVal 708
Db 1819 GGCACCCAGCTTACCGAGTCTCTGAGAGGAGGAGTGCATGCTGGACCCAGCGCTGTG 1878
Oy 709 GluAspGlyThrProCysGlyProSerMetCysLeuAspArgLysCysLeuGlnIle 728
Db 1879 ATGACTGGAACCAAGTGTGCTACAAACCATATTGCTTTGAGGGGCAAGTGCACAGAACCC 1938
Oy 729 GlnAlaLeuAsnMetSerSerCysProLeuAspSerLysGlyLysValCysSerGlyHis 748
Db 1939 TCCCTTTTGAACGTGAAGCTGT-----GGAGAAGATGCAATGCCCAT 1983
Oy 749 GlyValCysSerAsnGlnAlaThrCysIleCysAspPheThrTyrAlaGlyThrAspCys 768
Db 1984 GGGGTCTGTAAACAACACAGACATGCGCCTGCGGGGGGCGCCCTTCTGC 2043
Oy 769 SerIleArgAspProValArgAsnLeuHisProProLysAspGlyProLysGlyPro 788
Db 2044 AACACACCGGCGCACGGGCGCAGTATC-----GACAGTGGGCTTATGCCCCCT 2091
Oy 789 SerAlaThrAsnLeuIleIleGlySerIleAlaGlyIleLeuValAlaAlaIleVal 808
Db 2092 CAGAGTGTGGCTCTGTGTAAGTGTGATGCTGATGCTGCTGCTGCTGCTGCTGCTG 2151
Oy 809 Leu 809
Db 2152 Arg 2154

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Job time : 342 secs